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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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protein search, using sw model protein Š

April 25, 2006, 06:05:16 ; Search time 133.491 Seconds (without alignments) 82.286 Million cell updates/sec Run on:

US-10-764-428-1 120

1 QVQLVQSGAEVKKPGASVKVSCKAS 25 score: Sequence: Title: Perfect

Scoring table:

Gapop 10.0 , Gapext 0.5

2443163 Total number of hits satisfying chosen parameters:

2443163 segs, 439378781 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

summaries

A Geneseq 21:* geneseqp1980s:* Database :

geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:*geneseqp2001s:*geneseqp2002s:* geneseqp2004s:*geneseqp2005s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description			Adt88325 Human IL-	Adu80305 Heavy cha	Ady31444 Human ant	_		_	Ady31468 Human ant	Aar27045 Human hea		_		Adw87138 Anti-huma	Adx01239 Humanized	Adx27022 Human gro	Human	Ady31321 Human ant	Human	_	_	Ady59169 Anti-Tag-		Abr61972 Monoclona
đi	ADQ90697	ADU07258	ADT88325	ADU80305	ADY31444	ADY31447	ADY31453	ADY31459	ADY31468	AAR27045	AAW79211	AAE19676	AAU70462	ADW87138	ADX01239	ADX27022	ADY31315	ADY31321	ADY31327	ADY31312	ADY31336	ADY59169	AEB13671	ABR61972
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% Query Match Length DB	25	25	25	25	25	25	25	25	25	30	30	30	30	30	30	30	30	30	30	30	30	30	30	32
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Abr57347 MatDC16 V Abo55410 Human gen Abo5987 Human gen Abo70846 Human yar		Abj18729 VH antibo Abg75309 Human Bub Abm79521 Human DP7		Adf09867 Anti-MC1 Aar57475 Human HV3 Aar92078 Human HV3 Abg31425 Amino aci Aay50952 Human ant
ABR57347 ABO55410 ABO55987	ABCZ0856 ADX18820 ABJ18728 ABJ18731	ABJ18729 ABG78309 ABM79521	AAK92991 ABG78172 ABG91863 ADC99825 ADD05429	ADF09867 AAR57475 AAR92078 ABG31425 AAY50952
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ALIGNMENTS

AD090697 standard; peptide; 25 AA.

ADQ90697;

(first entry) 21-OCT-2004 Anti-VEGF antibody heavy chain FR1 subgroup I peptide SEQ ID NO:1.

antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antiinflammatory; antianglogenic; immunomodilatory; antibody therapy; tumour; inflammatory disorder;; angiogenic disorder; imflammatory disorder; anti-VEGF antibody; anti vascular endothelial cell growth factor antibody; heavy chain; FRI.

Homo sapiens Synthetic. WO2004065417-A2.

05-AUG-2004.

23-JAN-2004; 2004WO-US001844.

23-JAN-2003; 2003US-0442484P.

(GETH) GENENTECH INC.

Simmons L;

WPI; 2004-562149/54.

Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.

Claim 15; SEQ ID NO 1; 161pp; English.

The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid

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The antibody or antigen binding fragment variable domain.

The antibody or antigen binding fragment variable domain comprises the modified FR that has improved yield in cell culture compared to an undofified antibody or antigen-binding fragment. The antibody and antigen binding fragment or antigen-binding fragment. The antibody and antigen binding fragment antibody and antigen binding fragment antibody and antigen confoured in antibody therapy. The methods and compositions of the present invention are useful for producing antibodies or antigen binding fragments in cell culture, in barticular for improving the yield of recombinant antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and inflammatory, angiogenic and immunological disorders. The present celecter represents a heavy chain FRI peptide of an anti-VEGF (vascular endothelial cell growth factor) antibody, which is used in the exemplification of the present invention.
                       the amino acid found at the corresponding FR position of a human subgroup variable domain consensus sequence that has a hypervariable region 1 (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
a different amino acid, where the different
   position with
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Sequence 25 AA;

ö Length 25; 0; Indels 100.0%; Score 120; DB 8; 100.0%; Pred. No. 4.2e-10; iive 0; Mismatches 0; 25 1 QVQLVQSGAEVKKPGASVKVSCKAS 25 QVQLVQSGAEVKKPGASVKVSCKAS Query Match
Best Local Similarity 100...
Lines 25; Conservative ઠ 셤

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Gaps

RESULT 2

ADU07258 standard; peptide; 25 AA. ADU07258; ADU07258

IL-9 antibody variable heavy chain (VH) framework region 1 sequence #1. (first entry) 13-JAN-2005

Respiratory infection; human; interleukin-9 antagonist; IL-9; respiratory syncytial virus; anti-RSV antigen antibody; leukotriene modifier; asthma-like symptom; wheezing; allergy; immunomodulatory; anti-inflammatory; anti-irial; antibiotic; antifungal; mast cell modulator; virucide; antibacterial; fungicide; antiathatic; antiallergic; IL-9 antibody; variable heavy chain; VH; framework region.

Homo sapiens

WO2004091519-A2

12-APR-2004; 2004WO-US011329. 28-OCT-2004.

11-APR-2003; 2003US-0462307P. 10-JUN-2003; 2003US-0477801P.

(MEDI-) MEDIMMUNE INC

Reed JL;

NPI; 2004-775524/76.

Managing, treating or ameliorating in a human subject a respiratory infection or its symptoms caused by bacteria, fungi or respiratory syncytial virus by administering an IL-9 antagonist.

Disclosure; SEQ ID NO 33; 276pp; English.

The invention relates to a method of managing, treating or ameliorating a respiratory infection or its symptom in a human subject by administering

an interlemental of the subject an anti-respiratory syncytial virus (anticompanies antibody. The anti-RSV antigen antibody is palivizumeb. The
method futther comprises administering a leukotriene modifier, which is
method of preventing the development, onset or progression of asthma or
one or more asthma-like symptoms in a child, a method of preventing,
one or more asthma-like symptoms in a child, a method of preventing,
or child, a method of preventing wheezing in a pre-term infant, infant
or child, a method of preventing, managing, treating or ameliorating asthma or an alleray or its symptoms in a human subject. and a method of preventing, managing,
treating or ameliorating asthma or an alleray or its symptoms in a human subject. Preventing in a human subject, once asthma-like symptoms in a child having or previously having a subject. Preventing the development, onset or progression of asthma or
one or more asthma-like symptoms in a child having or previously having a respiratory infection comprises administering an IL-9 antagonist. The
contact of thild comprises administering an IL-9 antagonist. The
infant, infant or child comprises administering in a lugan subject comprises administering or ameliorating wheezing in a human subject comprises administering or an il-9 antagonist. The definition of an IL-9 antagonist. The method further comprises administering or a matiinflammatory agent, an anti-viral agent, an anti-interior or a mast call modulator. The method further comprises
administering to the subject a leukotriene modifier, an anti-interior administering an IL-9 antagonist and an least one other antibody, an anti-interior and anti-interior an anti-interior and anti-interior and anti-interior and anti-y antagonist and an antibody, an anti-interior and anti-interior and anti-y antagonist and an anti-pass in an anti-y antagonist and an anti-pass in an anti-pass in an anti-pass in an anti-pass in Sequence 25 AA; against

ö Gaps ö 100.0%; Score 120; DB 8; Length 25; 100.0%; Pred. No. 4.2e-10; Indels 0; Mismatches 25; Conservative Best Local Similarity Matches 25; Conserv Query Match

1 QVQLVQSGAEVKKPGASVKVSCKAS 25 QVQLVQSGAEVKKPGASVKVSCKAS 25 ઠે 셤

ADT88325

ADT88325 standard; peptide; 25 ADT88325;

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(first entry) 13-JAN-2005

Human IL-19 antibody VH framework region 1 seqid 33.

respiratory; antiinflammatory; immunosuppressive; antiasthmatic; antiallergic; antiarthritic; neuroprotective; antirheumatic; immunotoxin; antiallergic; antianthistor; TNR alpha antagonist; IL-9 antagonist; IL-9; antibody; 4D4; 4D4; 4D4 H2-1 D11; 4D4com-XF9; 4D4com-2F9; 7F3; 7TA10; 22D3; 7F3com-2H2; 7F3com-3H5; 7F3com-3D4; IL-9 associated disorder; respiratory infection; respiratory syncytial virus; parainfluenza virus; human metapneumovirus; inflammatory disorder; asthma; allergy; arthritis; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tramework region 1; variable heavy chain.

Homo sapiens

WO2004091510-A2.

28-OCT-2004

12-APR-2004; 2004WO-US011172.

ä Ondek

Marquis DM, Allan BW,

Reed JL;

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The invention describes a new composition comprising a CD20 binding molecule having a binding affinity (Kd) for human CD20 of 5.0 x 10 -10 M or less, and a dissociation rate (Koff) for human CD20 of 5.0 x 10 -4 s-1 or less, Also described is a method of treating B cell lymphoma. The CD20 binding molecules are useful for preparing a composition for treating B cell lymphoma. This is the amino acid sequence of human heavy chain framework region VHI DP7/21-2 FRL1 used in the creation of a CD20 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising a CD20 binding molecule having a binding affinity (Kd) for human CD20 and a dissociation rate (koff) for human, useful for preparing a composition for treating B cell lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 95; 84pp; English.
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                                                                                                                                                                                                                     (MOLE-) APPLIED MOLECULAR EVOLUTION
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                                   20-MAY-2004; 2004WO-US015786.
                                                                                                      20-MAY-2003; 2003US-0471958P
                                                                                                                                                  52US-00471958
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nes 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a new IL-9 antibody comprising: a variable heavy CC (WH) or variable light (VL) domain having an amino acid sequence of the VH or VL domain of 4D4, 4D4 H2-1 D11, 4D4ccm-XF9, 4D4ccm-ZF9, 7F3, 7D40, 22D3, 7P3ccm-2H2, 7F3ccm-3H5 or 7F3ccm-3H5 or 7F3ccm-3H5 or 7F3ccm-3H5 or 7F3ccm-3H5.

CC 22D3, 7P3ccm-3H5 or 7F3ccm-3H5, 7D4 or a complementarity of 4D4 H2-1 D11, 4D4ccm-XF9, 4D4ccm-ZF9, 7F3, 7LA10, 22D3, 7F3ccm-2H2, 4D4 CC C F3ccm-3H5 or 7F3ccm-3H5.

CC 7F3ccm-3H5 or 7F3ccm-3H5. The antibody immunospecifically binds to a comprising the IL-9 antibody and a carrier; a method for preventing, comparising the IL-9 antibody and a carrier; a method for preventing, comparising the IL-9 antibody and a carrier; a method for preventing, a describing the aberrant expression or activity of an IL-9 polypeptide or an IL-9F, a comprising the contained within the packaging material and an article of manufacture comprising a packaging material and a carrier. The IL-9 pharmaceutical agent contained within the packaging material, where the pharmaceutical agent contained within the packaging material, where the pharmaceutical agent comprises the IL-9 antibody and a carrier. The IL-9 pharmaceutical agent comprises the IL-9 antibody and a carrier. The IL-9 contained within the packaging material, where the pharmaceutical agent comprises the IL-9 antibody and a carrier. The IL-9 crivity of an IL-9 polypeptide or an IL-9F, e.g., respiratory infection caused by bacteria or respiratory syncytial vitus, parainfinenza vitus or human metapneumovirus, inflammatory disorder such as sthmia, allergy or arthritis or autoimmune disorder such as rheumatoid arthritis and multiple sclerosis. This is the amino acid sequence of a human IL-19 mining fermine acid 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                           New IL-9 antibody comprising a variable heavy or light domain or a complementarity determining region having an amino acid sequence of e.g., 4D4, useful in treating or preventing e.g., respiratory infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                           11-APR-2003; 2003US-0462259P.
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Les 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disorder.
                                                                                                                                                              (MEDI-) MEDIMMUNE INC.
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Indels

100.0%; Score 120; DB 8; 100.0%; Pred. No. 4.2e-10; tive 0; Mismatches 0;

Length 25;

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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
                                                             DNA library; humanized antibody; antibody engineering; heavy chain.
Human antibody heavy chain framework peptide - SEQ ID 276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 276; 179pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Damschroder M;
                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2003; 2003US-0497213P.
13-OCT-2003; 2003US-0510741P.
                                                                                                                                                                                                                                                                                                                                        20-AUG-2004; 2004US-00923068
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therapy; antibody production; hematological disease; neoplasm; b-cell lymphoma; framework region; FRL1.

cytostatic; gene immune disorder;

WO2004103404-A1

02-DEC-2004

Homo sapiens.

Heavy chain framework region VHI DP7/21-2 FRL1.

ADU80305;

RESULT 4 ADU80305

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Query Match

Best Loc Matches

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Homo sapiens
                                                                                                                                            05-MAY-2005
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                 The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid sequence represents a human germline heavy chain framework
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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
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ADY31453 standard; peptide; 25 AA.
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The human framework sequence FR1 was used in the prodn. of humanised monoclonal antibodies comprising antigen binding sites (CDRs) of non human origen based on consensus sequence of CDRs. The sequence is a heavy chain framework region. The humanised antibodies or their chimeric variants may be used as therapeutic or diagnostic agents in order to combat e.g. glioma, melanoma or carcinoma. See also AAR27299-300 and AAR27037-51. (Updated on 25-MAR-2003 to correct PN field.)
light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework
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Pred. No. 4.2e-10;
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                                                                                                                                                                                                                                    Location/Qualifiers
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/label= Thr, Ser
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13-OCT-2003; 2003US-0510741P.
              20-AUG-2004; 2004US-00923068
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                                                                                                                                      H, Dall-Acqua W,
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Gaps

AAW79211;

RESULT 11

AAW7921

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The invention relates to an antibody molecule having specificity for human tumour necrosis factor-alpha (TNFalpha) comprising a heavy or light combined to the compound comprising the antibody is useful for treating or manufacturing a medicament for treating a pathology mediated treating or manufacturing a medicament for treating a pathology mediated diseases which can be treated by the antibody include sepsit, congestive conferences such can be expected by the antibody include sepsit, congestive conferences such cachexia, adult respiratory distress syndrome, acquired immunodeficiency syndrome (AIDS), allergies, consensis, inflammatory bone disorders, blood coagulation disorders, burns, rejection episodes following organ or tissue transplant, Crohn's disease and autoimmune diseases, such as thyroiditis. The antibodies may also be used to reduce the side effects associated with TNFalpha generation during neoplasty therapy, to eliminate or reduce shock-related symptoms associated with the treatment or prevention of graft rejection by use of an anti-lymphocyte antibody, for treating multicorregan failure, or in the diagnosis and imaging of disease states involving elevated levels of TNF alpha. The present sequence is human cross group I consensus peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody specific for human tumor necrosis factor (TNF)-alpha, useful for treating TNF-alpha-mediated diseases, e.g. congestive heart failure, septic or endotoxic shock, cachexia, adult respiratory distress syndrome.
                  Human; tumour necrosis factor 40; TNF40; osteopathic; cardiant; CDR; complementarity determining region; rheumatoid; osteo-arthritis; sepsis; congestive heart failure; shock; tissue transplant; tuberculosis; ADDS; Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome; acchexia, allergy; psoriamis; blood coagulation disorder; thyroiditis; inflammatory bone disorder; Crohn's disease; autoimmune disease; burn; neoplasty therapy; immunomodulator; vulnerary; graft rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 120; DB 5; Length 30; 100.0%; Pred. No. 5e-10; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weir ANC, Popplewell AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
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                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2001; 2001WO-GB002477.
                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-2000; 2000GB-00013810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CELL-) CELLTECH R & D LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-216732/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30 AA;
                                                                                                                                                                                                                                                                        WO200194585-A1
                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                         13-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Athwal DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU70462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   King DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This represents the amino acid sequence of the framework 1 region of human antibody clone Amu 5-3. This is used to construct a humanised antibody LO-CD2a. The invention relates to the use of the memoclonal antibody (MAD) LO-CD2a or a humanised or a chimeric version of the LO-CD2a antibody for the inhibition of a T-cell mediated immune response in a patient. The MAD LO-CD2a (produced by hybridoma cell) line ATCC HB 11423) can bind to an epitope on the CD2 antigen of the human lymphocytes. The T-cell mediated immune response in a patient can be inhibited by administering the MAD LO-CD2a or an antibody that binds to the same human lymphocyte epitope as LO-CD2a or an antibody that binds to preventing transplant rejection or for treating graft-versus-host disease or for treating graft-versus-host disease
                                                                                                                                                                                                                                                                                             Monoclonal antibody; MAb; LO-CD2a; humanised antibody; CD2 antigen; human lymphocyte; immune response; chimeric; graft-versus-host disease; T-cell; transplant rejection; autoimmune disease; Amu 5-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibition of T-cell mediated immune response with anti-CD2 monoclonal antibody LO-CD2a - used for preventing transplant rejection or for treating graft-versus-host disease or auto-immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                Framework 1 region of human antibody clone Amu 5-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7; Col 35-36; 96pp; English.
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                                                                                               AAW79211 standard; protein; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE19676 standard; peptide; 30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYLO-) UNIV CATHOLIQUE LOUVAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-00027008.
93US-00119032.
95US-00407009.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-556337/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
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                                                                                                                                                                                                  21-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-SEP-1993;
29-MAR-1995;
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Gaps

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AAE19676;

AAE19676
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Query Match Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polymucleotides encoding different immunoglobulin binding protein (1989) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polymeptides in transformed plant cells are selected, and preparing an IgBP array in plant cells. At least one peptide sequence has at least 75% sequence identity to a framework region (RR) of a native 1gM, 1gG, 1gA, sequence identity to a framework region (RR) of a native 1gM, 1gG, 1gA, 1geful for preparing an immunoglobulin molecule. The method is cusful for preparing an immunoglobulin binding protein array, preferably chany chain binding protein (CHB) array in eukaryotic cells especially cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening assays of 1gBPs having desired characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an 1gBP of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for preparing array.
complementarity determining region; framework region; IgBP;
transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
IgD; IgB; IgY; IgM; kappa; lambda; CHBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody engineering; antiasthmatic; dermatological; antiallergic; antinflammatory; gastrointestinal-gen.; cytostatic; immunostimulant; diagnosis; interleukin-13; heavy chain variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 120; DB 5; Length 30; 100.0%; Pred. No. 5e-10; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1B; 129pp; English,
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                                                                                                                                                                                                                                                                            02-MAY-2001; 2001WO-US014349.
                                                                                                                                                                                                                                                                                                                             02-MAY-2000; 2000US-00563222.
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                                                                                                                                                                                                                                                                                                                                                                               (RPIC-) EPICYTE PHARM INC
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nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-055482/07
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiatt AC, Hein MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30 AA;
                                                                                                                                                                   WO200183806-A1.
                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-APR-2005
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Matches
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ID ADW87138

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Homo sapiens

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The invention relates to an isolated specific binding molecule (I) for human interleukin (IL)-13, comprising an antibody antigen-binding domain site composed of human antibody WH and VL domain comprising a set of complementarity determining regions (DRS) HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, (I) is useful for in vitro binding of (I) to human IL-13 or its fragment. and further involves determining the amount of binding of (I) to IL-13 or its fragment. (I) is useful in the manufacture of a medicament for treatment of a disease or disorder chosen from asthma, atopic dermatitis, allergic rhinitis, fibrosis, inflammancory bowel disease and Hodgkin's lymphoma. (I) is useful in disgnosing diseases such as asthma, atopic dermatitis, in the subject. (I) preferably neutralizes human IL-13. This sequence corresponds to protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated specific binding molecule for human interleukin-13, having antibody antigen-binding domain site composed of human variable heavy and light chain domains with complementarity determining regions, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody engineering; antibody production; immunosuppressive; immunotherapy; heavy chain variable region; light chain variable region; graft rejection; graft versus host disease; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                            Shorrock CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanized antibody generation peptide #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 27; 192pp; English.
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                                                                                                                                                                                                                                                            (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKAS
                                                                                                                                                                                                                                                                                                            Minter RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADX01239 standard; peptide; 30 AA
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                                                                                                                                                         31-MAR-2004; 2004GB-0007315.
31-MAR-2004; 2004US-0558216P.
24-MAY-2004; 2004US-0573791P.
                                                                                        15-JUL-2004; 2004GB-00015857
                                                                                                                                          2003US-0487512P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                 Jermutus L,
                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-104209/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30 AA;
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18-JUL-1997;
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                                                                                                                                          15-JUL-2003;
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GB2403952-A
                                             19-JAN-2005
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Bazin H, Latinne D, Kaplan R, Kieber-Emmons T,
White-Scharf ME;
(UYLO-) UNIV CATHOLIQUE LOUVAIN. (BIOT-) BIOTRANSPLANT INC.
                                                                                                                                            WPI; 2005-129962/14.
```

Postema CE;

The invention relates to a humanized antibody comprising the CDRs from LO-CD2a, produced by the cell line deposited as American Type Culture Collection (ATCC) HB11423, the humanized antibody containing in the framework of the heavy chain variable region of the humanized antibody, amino acids 47,67,70,72,76,85, and 87, and one, two, three, or four of amino acids 12, 13, 28, and 48 of the rat LO-CD2a heavy chain variable region of 118 amino acids, fully defined in the specification. The antibody is useful for preventing or inhibiting graft rejection, graft versus host disease or autoimmune disease. This sequence corresponds to a peptide used in the invention. New humanized antibody comprising the complementary determining regions (CDRs) from LO-CD2a, useful for preventing or inhibiting graft rejection, graft versus host disease or autoimmune disease. Example 7; SEQ ID NO 52; 126pp; English.

Sequence 30 AA;

Gaps ö Query Match 100.0%; Score 120; DB 9; Length 30; Best Local Similarity 100.0%; Pred. No. 5e-10; Matches 25; Conservative 0; Mismatches 0; Indels

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1 QVQLVQSGAEVKKPGASVKVSCKAS 25 QVQLVQSGAEVKKPGASVKVSCKAS 25 ઠ ద

Search completed: April 25, 2006, 06:15:07 Job time : 136.491 secs

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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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model 38 - protein search, using OM protein April 25, 2006, 06:15:41; Search time 21.2264 Seconds (without alignments) 113.322 Million cell updates/sec Run on:

US-10-764-428-1 120 1 QVQLVQSGAEVKKPGASVKVSCKAS 25 score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match O% Maximum Match 100% Listing first 45 summaries

PIR 80:* **Database**:

1: pirl:* 2: pirl:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	heavy	Ċ	leavy	eavy	leavy	eavy	eavy	eavy	neavy	leavy	neavy	neavy chain	neavy chain	eavy	Ig heavy chain V r	leavy	leavy	leavy	еалу	eavy	eav.	i-Sma	heavy chain V	heavy chain	heavy chain V	chain	heavy chain	heavy chain	Ig heavy chain V1
QI	826910	S26920	S26918	S26912	S26938	S26913	S26919	869899	S21925	S31667	HVHU35	HVHUHG	S18552	S31680	S18553	S18551	S36265	S36271	S19665	S46393	831596	S49530	A32483	829257	S34014	A30523	\$26915	\$24680	S46463
DB	~	~	~	~	~	N	~	~	~	7	н	-	~	~	~	~	~	~	~	~	~	7	~	7	~	7	7	7	~
Length	86	98	98	98	98	98	98	104	111	116	117	117	117	117	117	117	118	122	124	129	132	135	142	148	127	98	98	98	98
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.3	97.5	97.5	97.5	•
Score	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	118	117	117	117	117
Result No.		N	9	4	S	9	7	00	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

heavy c	heavy chain heavy chain	heavy chain heavy chain heavy chain	Ig heavy chain V r Ig heavy chain V-1	Chain Chain Chain	Ig heavy chain V r Ig heavy chain V-1 Ig heavy chain pre
S31698 PH0959	G1HUEU PH0961	PH0962 PH0958 S44108	PH0957 B33548	PH0952 A33548 PH0954	S46394 C33548 B32274
0 0		0 0 0	000	•••••	000
116	117	120 122 122	125	128	132 133 135
97.5	97.5	97.5 97.5	97.5 87.5 8.5	97.79 97.79	97.5 97.5 97.5
117	117	117	1111	111	11111
30	33	35	38	2 4 4 4 2 0 1 0	444 640

ALIGNMENTS

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C.Species: Homo sapiens (man)
C.Species: Lono sapiens (man)
C.Accession: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C.Accession: 826910
R.Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Blol. 227, 776-798, 1992
A.Fitle: The repertoire of human germline V(H) sequences reveals about fifty groups of V. A.Fitle: The repertoire of human germline V(H) sequences reveals about fifty groups of V. A.Fatus: preliminary
A.Status: preliminary
A.Status: preliminary
A.Residues: 1-98 <70M>
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI00001163FA; EMBL:Z12303; NID:g32847; PIDN:CAA78173.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
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Ig heavy chain V region (DP-1) - human (fragment)
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1 QVQLVQSGAEVKKPGASVKVSCKAS 25 1 QVQLVQSGAEVKKPGASVKVSCKAS 25 g 8

RESULT 2 826920 Ig heavy chain V region (DP-7) - human (fragment)

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 826920
J; Mol. Biol. 227, 776-798, 1992
J;Reference number: S26895; MUID:93021117; PMID:1404388
J;Reference number: S26895; MUID:93021117; PMID:1404388
J;Reference number: S26920
J;Reference number: Number

Gaps ö Length 98; Indele Query Match
100.0%; Score 120; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 25; Conservative 0; Mismatches 0;

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1 QVQLVQSGAEVKKPGASVKVSCKAS 25

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A;Cross-references: UNIPARC:UP1000011644A, EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992 (S.Superfamily: immunoglobulin V region; immunoglobulin homology (S.Superfamily: immunoglobulin Rimanoglobulin Pils-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession. S26913
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
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C; Species: Lower 1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Jaces 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S26919
R; Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
J; Mol. Biol. 227, 776-798, 1992
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A; Reference number: S26885; MUID:93021117; PMID:1404388
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Pred. No. 1.9e-10;
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; Pred. No. 1.9e-10;
0; Mismatches 0;
                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 25; Conservative 0; Mismatches 0;
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Ig heavy chain V region (DP-14) - human (fragment)
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100.0%; Score 120; Di
Best Local Similarity 100.0%; Pred. No. 1.9
Matches 25; Conservative 0; Mismatches
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Best Local Similarity 100.0%;
Matches 25; Conservative 0
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A; Residues: 1-98 <TOM>
      1-98 <TOM>
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A;Residues: 1-98 <TOM>
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A;Status: preliminary
A;Nolecule type: DNA
A;Reatdus: 1-98 <TONA
A;Reatdus: 1-98 <TONA
A;Cross-references: UNIPARC:UPI000031F36; EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID
C;Superfamally: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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36938
19 heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: A. M. Homo sapiens (man)
C;Accession: S26938
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The reperiorire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26938
A;Accession: S26938
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Igheavy chain V region (DP-8) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-NOV-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26912
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885, MUID:93021117; PMID:1404388
                                                                                                                                                                          Igheavy chain V region (DP-15) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 22-NOv-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S2698
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J, Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
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25; Conservative
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A Molecule type: DNA
A Residues: 1-98 <TOM>
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Matches
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Length 116;

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Query Match
100.0%; Score 120; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 25; Conservative 0; Mismatches 0;
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A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
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A,Nolecule type: mRNA
A,Residues: 20-116 <MAR>
A,Cross-references: UNIPARC:UPI000017372B
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                                                                                                                                                           19 QVQLVQSGAEVKKPGASVKVSCKAS
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$31667
Ig heavy chain V region - human
C; Species: Homo sapiens (man)
C; Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: 331667
R; Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A; Deference number: 31585
A; Accession: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: 31585
A; Accession: 331667
A; Residues: 1-116 < CUI>
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-116 < CUI>
A; Cross-references: UNIPARC: UPIO00011647F; EMBL: Z14215; NID: 337799; PIDN: CNA78584.1; PIL
C; Superfamily: immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
P; 33-116/Domain: immunoglobulin homology < LMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region - human

[Species: Homo sapiens (man)

[C;Species: Homo sapiens (man)

[C;Species: Homo sapiens (man)

[C;Species: Homo sapiens (man)

[C;Species: Orebe-1995 #sequence_revision 20-Peb-1995 #text_change 23-Jul-1999

[C;Species: 20-Peb-1995 #sequence_revision 20-Peb-1995 #text_change 23-Jul-1999

[C;Species: Day A; Priedman, D.F.

[A;Reference number: $21923

[A;Refidues: preliminary

[A;Refidues: DAA

[A;Refidues: 1-11 < PRL>

[A;Cross-references: UNIPARC:UPIO000115FA1; EMBL:X60503; NID:g33626; PIDN:CAA43023.1; PII

[C;Genetics: 16/1

[C;Genetics: 16/1

[C;Genetics: 16/1

[C;Superfamily: immunoglobulin V region; immunoglobulin homology

[C;Keywords: heterotetramer; immunoglobulin]
                 Ig heavy chain V region (clone RPTS7H), rheumatoid factor - human (Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Date: 14-Peb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000 C;Accession: 869899 R;Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J Rur. J. Immunol. 23, 1220-1225, 1993 A;Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune responsation: 868899 A;Accession: 868899 A;Secession: 868899 A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-104 cRAM>
                                                                                                                                                                                                                                                                                                                                                                        A;Gross-references: UNIPARC:UP1000011664D; EMBL:234893; NID:9509803; PIDN:CAA84376.1; PI
C;Guperfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 120; DB 2; 100.0%; Pred. No. 2e-10;
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Matches 25; Conservative
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Matches 25; Conserv
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Gly heavy chain precursor V region (V35) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: S00476; S34013
C;Accession: S00476; S34013
EMBO J, 7, 1047-1051, 1988
A;Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain localization of D segments in the human immunoglobulin heavy-chain localization of D segments in the human immunoglobulin heavy-chain localization of D segments in the human immunoglobulin heavy-chain localization of D segments in the human immunoglobulin heavy-chain localization of D segments in the human immunoglobulin heavy-chain localization of D segments while the human immunoglobulin heavy-chain localization of D segments while the human immunoglobulin heavy-chain localization of D segments while the human immunoglobulin heavy-chain localization while the human immunoglobulin he
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A; Molecule type: DNA
A; Cross-references: UNIPROT: P23083; UNIPARC: UPI00001179DB; EMBL: X07448; NID: g33104; PIDN
A; Morte: the authors translated the codon AGT for residue 89 as Met
B; Mariette, X.; Tsapis, A.; Brouet, J.C.
B; Mariette, X.; Tsapis, A.; Brouet, J.C.
A; Mariette, X.; Tsapis, A.; Brouet, J.C.
A; Mille: Nucleotidic sequence analysis of the variable domains of four human monoclonal
A; Reference number: $34001; MUID: 93209281; PMID: 7681398
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R;Rechavi, G.; Ram, D.; Glazer, L.; Zakut, R.; Givol, D.
R;rechavi, G.; Ram, D.; Glazer, L.; Zakut, R.; Givol, D.
R;rechavi, G.; Ram, D.; Glazer, L.; Zakut, R.; Givol, D.
A;Title: Evolutionary aspects of immunoglobulin heavy chain variable region (V-H) gene A;Reference number: A02024; MUID:83144028; PMID:6298778
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C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (V35) #status predicted <WAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-117 <REC>
A; Residues: 1-117 <REC>
A; Cross-references: UNIPROT: P01743; UNIPARC: UPI000012CEE1
A; Note: the sequence was determined from the germline gene
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A,Map position: 14q32.33-14q32.33
A;Introns: 16/1
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C, Genetica:
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S31680

Gibeavy chain V region - human

Gispecies: Homo sapiens (man)

Gispecies: Homo sapiens

Gispecies: Jama-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

Gispecies: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

Submitted to the EMBL Data Library, June 1992

Aipescription: Mechanisms that generate human immunoglobulin diversity operate from the Aiperence number: S31589

Aiseins preliminary

Aiseins preliminary

Aiseins Preliminary

Aiseins 1-117 <CUI>
Aiseins 1-117 <CUI
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Ig heavy chain V region precursor (VI-3) - human (fragment)

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999

C; Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999

C; Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999

R; Shin, E.K.; Mateuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H

EMBO J. 10, 3641-3645, 1991

A; Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl

A; Reference number: $18551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Cross-references: UNIPARC:UP10000115FBB; EMBL:X62107; NID:937833; PIDN:CAA44017.1; PIU
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V-I region (HG3) #status predicted <WAT>
F;30-117/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-3) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                      Length 117;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                             Indels
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100.0%; Pred. No. 2.2e-10;
tive 0; Mismatches 0;
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100.0%; Pred. No. 2.2e-10;
tive 0; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-117 <SHI>
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Best Local Similarity 100.
Matches 25; Conservative
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C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence_revision 06-Jan-1997 #text_change 23-Jul-1999
C; Accession: S18553; S26916
E; Shin, E. K.; Matsuda, F.; Nagaoka, H.; Pukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Hc EMBO, J. 10, 3641-3645, 1991
A; Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: clt. A; Reference number: S18551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UDI0000176E84; EMBL:X62109
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V.
A;Reference number: S26885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 20-117 <TOM>
A;Cross-references: UNIPARC:UP10000116402; EMBL:Z12327; NID:g32871; PIDN:CAA78197.1; PID
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;1-19/Domain: signal sequence #status predicted <SIG>
P;20-117/Product: Ig heavy chain V region (VI-3b) #status predicted
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                      Ig heavy chain V region precursor (VI-3b) - human (fragment)
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100.0%; Pred. No. 2.2e-10;
tive 0; Mismatches 0;
20 QVQLVQSGAEVKKPGASVKVSCKAS 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S18553
A;Status: translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.09
Matches 25; Conservative
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 25, 2006, 06:05:44 , Search time 133.491 Seconds (without alignments) 132.131 Million cell updates/sec Run on:

US-10-764-428-1 120 1 QVQLVQSGAEVKKPGASVKVSCKAS 25 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 Total number of hits satisfying chosen parameters:

2166443 segs, 705528306 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_gprot:*
2: uniprot_trembl:* Lagabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					SUMMAKIBS	
Result		Query				•
		Match	Match Length	80	ID	Description
-	120	100.0	117	н	HV1B HUMAN	P01743 homo sapien
7	120	100.0	117	٦	HV1G HUMAN	
m	120	100.0	159	~	Q96QS0 HUMAN	homo
4	120	100.0	200	~	Q6N091 HUMAN	homo
S	117	97.5		Н	HV1A HUMAN	homo
v	117	97.5	120	~	Q6NSA4 HUMAN	Q6nsa4 homo sapien
7	117	97.5		~	Q6PJF1_HUMAN	homo
60	117	97.5	498	~	Q6N041 HUMAN	homo
•	116	vo		~	Q9Y298 HUMAN	рошо
10	114	ம		7	Q9UL94 HUMAN	homo
11	114	95.0		~	Q9UL92 HUMAN	homo
12	114	95.0		7	OPUL95 HUMAN	рошо
13	114	95.0	244	~	Q652C8 HUMAN	homo
14	113	94.2	52	~	Q96QR9 HUMAN	
15	112	93.3	4	7	Q6P089_HUMAN	homo
16	112	93.3		N	QSEBM2_HUMAN	hom
17	111	92.5	119	N	Q9GYZ2_MOUSE	Q9gyz2 mus musculu
18	110	91.7	125	7	Q6PILO_HUMAN	homo
19	110	91.7	147	-	HV1C HUMAN	рошо
70	109	90.8		~	Q6N030_HUMAN	homo
21	108	90.0		~	Q7Z7P5_HUMAN	homo
22	107	89.5		ч	HV1D HUMAN	homo
23	107	89.2		ч	HV1B HUMAN	homo
24	107	89.2		~	095978 HUMAN	homo
25	105	87.5		~	Q569B1_RAT	ratto
56	104	86.7	475	~	Q6N095 HUMAN	homo
27	103	85.8		~1	HV1F HUMAN	P06326 homo sapien
28	103	85.8		~	Q9D8L4 MOUSE	mus n
29	103	82.8		~	Q96DK0 HUMAN	homo
30	103	85.8		N	QEMZWO HUMAN	hom
31	102	85.0	484	7	Q99LA6_MOUSE	Q99la6 mus musculu

Q8wy24 homo sapien Q4kml5 mus musculu Q8vdc9 mus musculu Q6zp87 homo sapien Q5bk05 rattus norv Q6pjb2 mus musculu Q5fvp3 rattus norv Q91wt1 mus musculu Q4qqw0 rattus norv Q8vcx7 mus musculu Q5bjz2 rattus norv Q5bjz2 rattus norv Q9ul89 homo sapien Q9d9b8 mus musculu
2 Q8WY24_HUMAN Q4KML5_MOUSE Q6ZP87_HUMAN Q5BKO5_RAT Q6PJB2_MOUSE Q6PJB2_MOUSE Q9JWT1_MOUSE Q6QW0_RAT Q8BJZ2_RAT Q6BJZ2_RAT Q9BJSS_Q9UL89_HUMAN
617 617 168 208 458 458 445 613 458 116
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
1001 1001 1001 1001 1001 1001 1001
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## ALIGNMENTS

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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                        Best Local Similarity
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                                                   NCBI_TaxID=9606;
                                                                                      Tilson M.D
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                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMML outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                   01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
110-MAY-2005 (Rel. 47, Last annotation update)
119 heavy chain V-I region V35 precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                              Mariette X., Tsapis A., Brouet J.C., "Nucleotidic sequence analysis of the variable domains of four human monoclonal IgM with an antibody activity to myelin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINES #8926408; PubMed=2841108;
Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
Ohno H., Fukuhara S., Honjo T.;
Dispersed localization of D segments in the human immunoglobulin
heavy-chain locus.";
EMBO J. 7:1047-1051(1988).
                                                                                                                                                                                                                                                                                                                           Eur. J. Immunol. 23:846-851(1993).
-1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 120; DB 1; Length 117; 100.0%; Pred. No. 1.2e-10;
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Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Immunoglobulin domain; Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 117 IG heavy chain V-I region 120 ×117 Ig-like. 117 117 AA; 13009 MW; BEGICEGIFBCE97BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X07448; -; NOT ANNOTATED_CDS; Genomic_DNA.
PIR; S00476; HVHU35.
HSSP; PO1751; HOUG.
SMR; P23083; Z0-117.
Ensembl; ENSG00000130076; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular region; NAS. GO: 0003823; F:antigen binding; NAS. GO; GO:000555; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                 PRT;
                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE OF 20-116.
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Q96QSO;
01-DBC-2001 (TEMBLEE] 19,
01-DBC-2003 (TEMBLEE] 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 25; Conservative
                                 STANDARD;
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                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                       PubMed=7681398;
                                                                                                                                                                                                                                                                                                                  glycoprotein.";
                               HV1G HUMAN
P23083;
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NON TER
SEQUENCE
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          RESULT 2
HV1G_HUMAN
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06.001,
05.0UL-2004 (TrEMBLrel. 27, Last sequence update)
05.0UL-2004 (TrEMBLrel. 27, Last annotation update)
05.0UL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686C02220 (Fragment).
Name-DKFZp686C02220,
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Human rectum tumor;

G The German Human cDNA Consortium;

G The German Human cDNA Consortium;

A Fobo G., Han M., Wiemann S.), Mewes H.W., Weil B., Amid C., Osanger A.,

B Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; BX646625; CAE45779.1; -; mRNA.

R SMR; Q6N031; 270-478.

R InterPro; IPR0031599; Ig.

R InterPro; IPR0031597; Ig.-1.

R InterPro; IPR0031597; Ig.-1.

R InterPro; IPR0031597; Ig.-1.

R InterPro; IPR0031597; Ig.-1.

R InterPro; IPR003166; Ig.-1.

R InterPro; IPR003166; Ig.-1.

R SMART; SM00409; IG; 4.

SMART; SM00406; IG: 4.

SMART; SM00406; IG.1.

R SMART; SM00406; IG. II.KE; 4.

R SMART; SM00406; IG. II.KE; 4.

R PROSITE; PS002209; IG_MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 100.0%; Score 120; DB 2; Length 159; l. Similarity 100.0%; Pred. No. 1.6e-10; 25; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 120; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 5.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                     Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                              EMBL, AX039025, AAK82649.1; -; MRNA.
HSSP, P01869; LAEG.
InterPro; IPR007110; Ig-like.
InterPro; IRR003596; Ig_v.
SMART; SM04406; IGv; 1.
Immunoglobulin domain.
SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 AA; 54160 MW; 3C423A17D65A41B4 CRC64;
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62

38 QVQLVQSGAEVKKPGASVKVSCKAS

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                               Ig heavy chain V-I region EU.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Biochemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gall W.B., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
Blochemistry 9:3188-3196(1970).
-!- MISCELLAMSOUS: The sequence of the gamma-1 C region of this myeloma protein has also been determined.
-!- SIMILARITY: Contains 1 1g-1ike (immunoglobulin-like) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-71064024; PubMed-5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;
                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P01751, 1A6W.
SMR; P01742; 1-102.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; P:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR00596; Ig-V.
                                                        117 AA
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OGNSA4;
05-JUL-2004 (TrEMBLrel. 27, Created)
                                                        PRT;
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MEDLINE-71064027; PubMed=4923144;
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                                                     STANDARD;
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                                                        HV1A_HUMAN
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RESULT 5
HV1A HUMAN
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Q6NSA4 HU
ID Q6NS,
AC Q6NS,
DT 05-J1
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RA KLEULES-COLEGE T. PubMed-12477932; DOI=10.1073/pnas.242603899;
RA KLEULINE=22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA KLEULINE=22388257; PubMed-1247, Groube L.H., Derge J.G.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RACHARGS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
R. Generation and initial analysis of more than 15,000 full-length human
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                             Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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WIM MGC Project;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC07033; AAH70333.1; -; mRNA.
HSSP; P01751; 1A6W.
SMR; GOSSA4, 21-116.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00406; IGV; 1.—
PROSITE; PSS0835; IG LIKE; 1.
Immunoglobulin domain.
SEQUENCE 120 AA; 13035 MW; 64620PAC874585D4 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) IGHV1-69 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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nes 24; Conservative
                                                                                 Homo sapiens (Human)
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TISSUE=Lung;
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HSSP; P01751; 1Abm.
SMR; Q6N041; 268-476.
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Q9Y298_HUMAN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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The German Human cDNA Consortium;
Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Mewes H.W., Well B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640710; CAE45829.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016381; AAH16381.1; -; mRNA.
HSSP; P01061; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686016217 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  498 AA
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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InterPro; IPR003110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_WHC.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 3.
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QGN041;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Ensembl; ENSG0000130076; Homo sapiens.
G0; G0:0015887; C:integral to plasma membrane; NAS.
G0; G0:0016066; P:cellular defense response (sensu Vertebrata); NAS.
InterPro; IPR00310; Ig-11ke.
InterPro; IPR00356; Ig-v.
ENART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Jacquemin M.G., Vander Blat L.P.L. VII Inactivation: study with an "Mechanism and kinetics of factor VIII Inactivation: study with an IgG4 monclonal antibody derived from a hemophilia A patient with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 498;
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Submitted (FRB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ24083; CAA11829.1; -; mRNA.
HSSP; P01867; HZH.
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150 150
150 AA; 16031 MW; 563D164AB22802D5 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 117; DB 2;
Pred. No. 1.5e-09;
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INTERPOSATION OF THE STATE OF T
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96.0%;
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Q9X298;
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les 24; Conservative
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Blood 92:496-506(1998).
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NON TER 1
SEQUENCE 498 AA; 5
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20 QVQLVQSGAEVKKPGASVKVSCKVS 44

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88277139; PubMed-9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                    MEDLINE=98277139; PubMed=9614914; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                     01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 AA; 13205 MW; 13E64P5345F4A16E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 114; DB 2;
92.0%; Pred. No. 1.1e-09;
tive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AP035022; AAD56286.1; -; mRNA.
HSSP; P01751; 1NQB.
Ensembl; ENSCO0000130076; Homo sapiens.
InterPro; IPR007110; Ig-like.
InterPro; IPR003566; Ig-v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                  Edul. Immunol. Immunopathol. 87:184-192 (1998).

EMBL; AF035020; AAD56256.1; -; mRNA.

HSSP; P01751; INQB.

HSSembl; ENSG00000130076; Homo sapiens.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

INTERFE; SN00406; IG-V.

PROSITE; PS50835; IG_LIKE; 1.
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              119 AA.
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               PRT;
                                         01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TERMBLrel. 13, Last seq
01-OCT-2003 (TERMBLrel. 25, Last ann
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Q9UL92;
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Best Local Similarity 92.0'
            QUL94 HUMAN PRELIMINARY;
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                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                                                                          Young D.C.;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Best Local Similarity 92.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 2; Mismatches 0; Indels
                                                                                                                               Length 124;
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MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain varlable region
                                                                                                                                                                                       0, Indels
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125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
                                                          124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
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Last annotation update)
                                                                                                                            Query Match
Best Local Similarity 92.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 2; Mismatches 0
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HSSP, P01751; INQB.
ENBendl; RNS000000130076; Homo sapiens.
InterPro; IPR07110; Ig-like.
InterPro; IPR07110; Ig-like.
SMART; SM00406; IGV; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last anno
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PROSITE; PS50835; IG_LIKE; 1.
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Q9UL95;
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Q6SZCB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment)
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                                                       NON TER
SEQUENCE
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1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                  ch 95.0%; Score 114; DB 2; Length 244; l Similarity 96.0%; Pred. No. 2.2e-09; 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 113; DB 2; Length 52;
Pred. No. 6.6e-10;
0; Mismatches 1; Indels
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EMBL, AX039026; AXR82650.1; -; mRNA.
HSSP; P01750; 1QNZ.
Ensembl; ENSG00000153613; Homo sapiens.
                                                                                                                                                                                                                                                                                      244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
Kontermann R.E., Wing M.G., Winter G.;
"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
EMBL; VIOUST; CANATSOO.1; -; MRNA.
InterPro; IPR003599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
SMART; SM00409; IG.; 2.
SMART; SM00409; IG.; 2.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 52 AA; 5560 MW; 838755B1D18CB976 CRC64;
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05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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Last annotation update)
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0960R9;

01-DEC-2001 (TrEMBLrel. 19, C:

01-DEC-2001 (TrEMBLrel. 19, L:

01-OCT-2003 (TrEMBLrel. 25, L:

Hypothetical protein.

Homo sapiens (Human).
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| Similarity 96.0%;
| Z4; Conservative
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0966R9 HUM
0966R8
AC 0960R
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DT 01-DE
DT 01-DC
DE HYPOT
OC BUKAR
OC BUKAR
OC HOMO
OC MAMMA
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RP TI180B
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haileh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Saress M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peress G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Radriquez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
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HSSP; P01751; 1A6W.
SNR; O67089; 250-458.
InterPro; IPR003109; Ig-like.
InterPro; IPR003599; Ig-like.
InterPro; IPR003599; Ig-like.
InterPro; IPR003596; Ig-wHC.
INTERPRO; IPR00396; IG-WHC.
INTERPRO; IPR004006; IG-WHC.
SWART; SW00409; IG-1.
FROSITE; PS50835; IG-LIKE; 4.
PROSITE; PS50835; IG-LIKE; 4.
Hypothetical protein.
SEQUENCE 480 AA; 51997 MW; ZE286C57E4F0ED65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSURE-Glandular pool- thyroid;
Strausberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Search completed: April 25, 2006, 06:24:39 Job time : 135.491 secs

us-10-764-428-1.rai

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NAME/KEY: Region
LOCATION: 30
OTHER INFORMATION: /note= "Amino acid 30 can be Thr or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 64191
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 30 amino acids
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    April 25, 2006, 06:25:05; Search time 33.7264 Seconds (without alignments) 61.284 Million cell updates/sec
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Sequence 2, P
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6_COMB.pep:*
(cgn2_6/ptodata/1/iaa/H_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-436-717-146
US-08-436-717-146
US-08-436-717-157
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US-08-291-16
US-09-254-180C-151
US-10-330-613A-54
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US-10-330-613A-54
US-US-95-10053-13
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                                                                                                                                                                                                     572060 seqs, 82675679 residues
                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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APPLICANT: Bendig, Mary M.
APPLICANT: Retrieborough, Catherine A.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Antibodies
INTER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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MEDIUM TYPE: Plopy disk

MEDIUM TYPE: Plopy disk

MEDIUM TYPE: Plopy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CLIASSIPLATION DATA:

APPLICATION NUMBER: US/07/946,421

FILING DATE: 06-NOV-1992

CLIASSIPLATION: A24

PRICA APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP92/00480

FILING DATE: 04-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 911933892

PRIOR APPLICATION DATA:

APPLICATION NUMBER: By 31,302

REGISTRATION NUMBER: 33,302

REGISTRATION NUMBER: MAR-1991

ATCHERPAN: 703-243-6410

TELEFRAN: 703-243-6410
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US-09-899-896-3
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US-09-515-697-90
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APPLICANT: TSUCHIYA, Masayuki
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: BALDANA, JOSES, Steven
APPLICANT: SALDANHA, JOSES,
ITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY
STREET:
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APPLICANT: SATO, Koh
APPLICANT: BENDIG, Wary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHABED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Weakington STATE: D.C. COUNTRY: USA ZIP: 2007-5109 COMPUTER RRADABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 152, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: WEGNER, Harold C. 288 REGISTRATION NUMBER: 25.288 REFERENCE/DOCKET NUMBER: 534 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-137-117D-146
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cacchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                 Query Match
100.0%; Score 120; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 15 inch diskette
COMPUTER: 16 inch diskette
COMPUTER: 16 inch diskette
COMPUTER: 16 inch diskette
CLASSIFATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-193
APPLICATION NUMBER: 08/027,008
FILING DATE: 09-SEP-193
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: 01stein, Ellict M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-146
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-08-137-117D-146
; Sequence 146, Application US/08137117D
                                                                                                                                                                                                                                                                                                                                                                 US-08-477-877B-52
; Sequence 52, Application US/08477877B
; Patent No. 5730979
                                              OTHER INFORMATION: Ser."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-477-877B-52
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US-07-946-421-11
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
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US-08-137-117D-157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: TSUCHINA, Masayuki
APPLICANT: TSUCHINA, Masayuki
APPLICANT: BRNDIG, Mary
APPLICANT: BRNDIG, Mary
APPLICANT: DONES, Steven
APPLICANT: BALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Mashington
STATE: D.C.
COUNTY: USA
ZIP: 20007-1109
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk.
                                                                                                                       COUNTEY. USA
ZIP: 2007-5109
COMPUTER READABLE PORM:
MEDIUM TYPE: 110ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
PILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25-2566
PROFEDENCY LOCKET NUMBER: 54-66
PROFEDENCY LOCKET NUMBER: 55-2566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
         CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLVQSGABVKKPGASVKVSCKAS 25
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
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Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-08-137-117D-152
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US-08-472-281A-52

Sequence 52, Application US/08472281A

Patent No. 5817311

Patent No. 5817311

Patent No. 5817311

Patent No. 5817311

APPLICANT: Latinne, Herv

APPLICANT: Latinne, Dominique

TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
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Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
OPERATING SYSTEM:
OPERATION SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION NUMBER: WO PCT/JP92/00544
FILING APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: 19 4-32084
FILING DATE: 19-FEB-1992
RIOR APPLICATION NUMBER: 26-358
FILING APPLICATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERBRAK: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSER: Carella, Byrne, Bain, Gilfillan, ADDRESSER: Cacchi, Stewart & Olstein STREET: 6 Becker Farm Road CITY: Roseland STATE: New Jersey COUNTR: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 18M PS/2
OMPUTER: 18M PS/2
OMPUTER: 18M PS/2
OMPUTER: 18M PS/2
OMPRATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,281A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INPORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
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. And St. C.

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; INFORMATION FOR SEQ ID NO: 1
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-436-717-146
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US-08-436-717-152
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TOPOLOGY:
US-08-436-717-152
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US-04-43-7/17-146

US-04-43-7/17-146

EAGUERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: SATOCHITA, MASAYUKI

APPLICANT: SATOCHITA, MASAYUKI

APPLICANT: SALDANHA, JOSE

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: 150

CONFERT SALON-510

CONFUTER READALE FOLDS, Learth STREET: JOSO K Street, N.W., Suite 500

CONFUTER: INFO COMPATION

COMPUTER: INFO COMPATIBLE

COMPATIBLE APPLICATION DATA:

APPLICATION NUMBER: US/08/436,717

FILING DATE: 24-APR-1992

REICR APPLICATION NUMBER: US/08/436,717

FILING DATE: 24-APR-1992

REICR APPLICATION NUMBER: US/08/436,717

REICR APPLICATION NUMBER: US/08/436,717

REICR APPLICATION NUMBER: US/08/436,717

APPLICATION NUMBER: US/08/436,717

APPLICATION NUMBER: US/08/436,717

REICR APPLICATION NUMBER: US/08/436,717

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REGISTRATION NUMBER: 25,258
REFERENCE TOOKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
RERERENCE/DOCKET NUMBER: 61750-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1740
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: alinear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLVQSGAEVKKPGASVKVSCKAS 25
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TELEX: 90
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SEQUENCE CRANCITES: 11.

JENGENEE STATUS: 1.

STANDEDURES: 11.00 of 1.

STANDEDURES: 11.00 of 1.

STANDEDURES: 11.00 of 1.

Guery Watch 1.

Beet Cool Similarity 100 of 1.

Beet Cool Similarity 100 of 1.

Beet Cool Similarity 100 of 1.

APPLICAT: 25

DD 1 QUQUAGGARTWACCHGNERKAR AS 5

RESULT 8

TITLE OF INVESTION STANDEDURES: 1.00

APPLICANT: SAND, School Assay AND APPLICANT: SAND, School Assay APPLICANT: School APPLICANT: School Assay APPLICANT: School
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STRANDEDNESS
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US-08-569-147-54
                                   JS-08-477-989B-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                           Gaps
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100.0%; Score 120; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
Query Match 100.0%; Score 120; DB 1; Length 30; Best Local Similarity 100.0%; Pred. No. 1.3e-10; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                  APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
STRPPF
STRPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PREENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
PILING DATE:
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 24-APR-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 78B-1991
ATTORNEY/AGENT INPORMATION:
NAME: WEGNER, HAROHG C
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
TELLEROWNINCATION INPORMATION:
TELLEROWNINCATION INPORMATION:
TELLEROWNINCATION INPORMATION:
TELLEROWS: (202) 672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3000 K Street, N.W., Suite 500 CITY: Washington COUNTY: D.C.
                                                                                  1 OVQLVQSGABVKKPGASVKVSCKAS 25
                                                                                                                   1 OVOLVOSGABVKKPGASVKVSCKAS 25
                                                                                                                                                                                                                  Sequence 157, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 904136
INFORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , TOPOLOGY: linear
US-08-436-717-157
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                                                                                                                                                                                                                  APPLICANT: Latinne, Dominique
APPLICANT: Kaplan, Ruth
APPLICANT: Kaber-Emmons, Thomas
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: White-Scharf, Mary
TITLE OF INVENTION: LO-CD2A Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEB: Carella, Byrne, Bain, Gilfillan,
ADDRESSEB: Cecchi, Stewart & Olstein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY CO
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Patent No. 5951983
GENERAL INFORMATION:
APPLICANT: Barin ...
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CITY: Roseland
STATE: New Jersey
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MOLECULE TYPE: polypeptide
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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: U.S.A.
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1 QVQLVQSGABVKKPGASVKVSCKAS
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US-09-830-748B-37
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                                                                                           RESULT 13
US-09-830-748B-37
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Fatent No. 6966620

Fatent No. 6966620

GENERAL INFORMATION:

APPLICANT: HINT, ANDEW C.

APPLICANT: HINT, MICH B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 06894-0501

CURRENT APPLICATION NUMBER: US/09/563,222C

FRIOR REPRING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

FRIOR PILING DATE: 2000-05-02
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                                                                                                                                                                                                                   COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,147
FILING DATE: 25-March-1996
ATTORNEY/AGENT INPORMATION:
NAME: TTUJIOL, DOTEON YALKO
REGISTRATION NUMBER: 35,719
REPERENCE/DOCKET NUMBER: 35,719
TELEPHONE: (215) 568-3100
TELEPACOMMATION INPORMATION:
TELEPACOMMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids

"WAND: AMINO acids
"WAND: AMINO ACIDS"
"WAND: AMINO ACIDS"
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                                                       ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6180377ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0;
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100.0%; Score 120; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-133
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as represented by The

APPLICANT: Secretary of the Department of Health and Human Services

APPLICANT: Rashmiri, Syed V.S.

APPLICANT: Padian, Eduardo A.

APPLICANT: Jeffery, Schlom

TITLE OF INVENTION: VARIANTS OF HUMANIZED ANTI-CARCINOMA MONOCLONAL ANTIBODY CC49

FILE REFERENCE: 4239-61725

CURRENT APPLICATION NUMBER: US/09/830,748B

CURRENT APPLICATION NUMBER: US/09/830,748B

CURRENT APPLICATION NUMBER: US 60/106,757

PRIOR APPLICATION NUMBER: US 60/106,757

PRIOR PILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60/106,534

PRIOR APPLICATION NUMBER: US 60/106,534

PRIOR APPLICATION NUMBER: US 60/106,334

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 37

LENGTHARE: PatentIn version 3.1

LENGTHE: 30
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APPLICANT: Bazin, Herv,
APPLICANT: Latinne, Dominique
APPLICANT: Raplan, Ruth
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: White-Scharf, Mary E.
APPLICANTON ION ION ENGINERY B.
TITLE OF INVENTION: 10.002 Antibody and Uses Thereof for Inhibiting T-Cell Activation
FILE REFERENCE: 61750-274
CURRENT APPLICATION NUMBER: 2000-06-26
PRIOR FILING DATE: 1997-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Framework 1 of heavy chain of
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100.0%; Score 120; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 120; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 OVOLVOSGAEVKKPGASVKVSCKAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLVQSGAEVKKPGASVKVSCKAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Society Application US/09462140D Patent No. 6849258 GENERAL INFORMATION:
Application US/09830748B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52
LENGTH: 30
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0; Gaps
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US-09-281-133

US-09-281-133

Sequence 133, Application US/09269921

Patent No. 669994

GENERAL INFORMATION:

APPLICANT: Onco, Koichiro

APPLICANT: Onco, Toshinko

APPLICANT: Yoshimura, Yasushi

APPLICANT: Koishimura, Yasushi

PILE REFERENCE: 35029-20007.00

TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY

FILE REFERENCE: 35029-20007.00

CURRENT PILING DATE: 1999-04-01

SEALIER APPLICATION NUMBER: US/09/269,921

CURRENT FILING DATE: 1999-04-01

SEALIER PILING DATE: 1999-04-01

SEALIER PILING DATE: 1996-10-03

RABLIER PILING DATE: 1996-10-04

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 133

LENGTH: 44
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CORGANISM: Unknown
CORGANISM: Unknown
FEATURE:
COTHER INFORMATION: Description of Unknown Organism: HG3
COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
COUNTY.

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Search completed: April 25, 2006, 06:28:39
Job time : 34.7264 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                      April 25, 2006, 06:58:17; Search time 108.962 Seconds (without alignments) 95.866 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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Sequence
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(gn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

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(gn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *

(gn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: *

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(gn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: *

(gn2_6/ptodata/1/pubpaa/US111_PUBCOMB.pep: *
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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Sequence 1, Application US/10764428
; Sequence 1, Application US/10764428
; Publication No. US20040223310A1
; BENERAL INFORMATION:
; APPLICANT: SImmons, Laura
; TITLE OF INVENTION: WIELD OF ANTIBODIES AND IMPROVING
; TITLE OF INVENTION: WIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
; TITLE OF INVENTION: CULTURE
; FILE REFERENCE: 11669-120USU1
; CURRENT PILING DATE: 2004-01-23
; FRIOR PILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 33
; SOCTHARE: PatentIn version 3.1
; SEQ ID NO 1.
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Sequence 33, Application US/1082353;
Publication No. US20050002934A1;
GENERAL INFORMATION:
APPLICANT RECAL JEANIER INFORMATION:
TITLE OF INVERTION: RECOMBINANT IL-9 ANTIBODIES AND USES THEREOF;
TITLE REFERENCE: 10271-112-999;
CURRENT APPLICATION NUMBER: US/10/823,253;
CURRENT PILING DATE: 2003-04-11;
PRIOR FILING DATE: 2003-04-11;
NUMBER: OF SEQ ID NOS: 60;
SEQ ID NO 33
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                                                                                                       US-10-699-874-21
US-09-609-804-21
US-10-81-904-130
US-10-032-037B-47
US-10-029-988B-47
US-10-029-926B-47
US-10-029-926B-47
US-09-158-120A-16
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US-10-125-687-17
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ORGANISM: Artificial Sequence
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US-10-823-253-33
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US-10-764-428-1
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                                                                                                                                                  ; Sequence 279, Application US/10923068; Publication No. US20050042664A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Homo sapiens
US-10-923-068-279
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US-10-923-068-285
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                                                                                                           Query Match 100.0%; Score 120; DB 5; Length 25; Best Local Similarity 100.0%; Pred. No. 1.8e-10; Matches 25; Conservative 0; Mismatches 0; Indels
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PUblication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Danschroder, Milliam
APPLICANTION INVENTION OF ANTIBODIES
FILE REFERENCE: AE600US
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 276
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                        Sequence 95, Application US/10849615
; Sequence 95, Application US/10849615
; Publication No. US20050025764A1
; GENERAL INFORMATION:
APPLICANT: Allan, Barrett W.
APPLICANT: Davies, Julian
APPLICANT: Ondek, Barlan
APPLICANT: Markins, Jeffry D.
APPLICANT: Watkins, Jeffry D.
71TLE OF INVENTION: CD20 BINDING MOLECULES
FILE REPERENCE: AME-09016
CURRENT APPLICATION NUMBER: US/10/849,615
CURRENT FILING DATE: 2004-05-20
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.3
SEQ ID NO 95
LENGTH: 25
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; LOCATION: (1)...(25)
; OTHER INFORMATION: FRH1 VkI (DP7/21-2)
US-10-849-615-95
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                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-823-253-33
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-923-068-276
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Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0;
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; Sequence 285, Application No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
APPLICANT: Dall'Acqua, William
; TILL OP INVERFICE 2004-09-20
; CURRENT FILING DATE: 2004-09-20
; SEQ ID NO 285
; LENGTH: 25
APPLICANT: WL. Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Damschroder, Melissa
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AE600US
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25
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Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Danschroder, Melissa
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AE600US
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1 QVQLVQSGAEVKKPGASVKVSCKAS
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Matches 25; Conserv
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GENERAL INFORMATION:
TITLE OF INVESTION: METHODS OF PREVENTING OR TREATING RESPIRATORY CONDITIONS
FILE REFERENCE: 10271-113-999
CURRENT APPLICATION NUMBER: 105/462,307
PRIOR PILING DATE: 2004-04-12
PRIOR PILING DATE: 2003-04-11
PRIOR FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VESTION 3.2
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100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0;
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Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: Mu, Herren
APPLICANT: Dall'Acqua, William
ITTLE OF INVENTION: HUMANIZATION OF ANTIBODIES
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FRELSEQ for Windows Version 4.0
SEQ ID NO 300
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 291
LENGTH: 25
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US-10-823-810-33
                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-10-923-068-291
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LENGTH: 25
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US-09-875-221A-95
                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Human group 1 consensus framework H1
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100.0%; Pred. No. 2.2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Athwal, Diljeet Singh
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Brown, Derek Thomas
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OP INVENTION: Biological Products
FILE REFERENCE: Carp-0089
CURRENT APPLICATION NUMBER: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2000-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
1 QVQLVQSGABVKKPGASVKVSCKAS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patentin version 3.1
SEQ ID NO 95
LENGTH: 30
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US-10-923-068-144
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Sequence 133, Application US/10783950

Bublication No. US20040199945A1

GENERAL INFORMATION:

APPLICANT: BPICYTE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

CURRENT APPLICATION NUMBER: US/09/563,222

PRIOR PELING DATE: 2004-02-19

PRIOR APPLICATION NUMBER: US/09/563,222

PRIOR APPLICATION NUMBER: PCT/US01/14349

PRIOR APPLICATION NUMBER: 09/563,222

PRIOR PELING DATE: 2000-05-02

PRIOR PELING DATE: 2000-05-02

NUMBER OF SEQ ID NOS: 182

SOFTWARE PLECTION NUMBER: 2000-05-02

NUMBER OF SEQ ID NOS: 182

SOFTWARE PRECENTIN Ver. 2.1

SEQ ID NO 133

LENGTH: 30

TYPE: RT
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                                                                                                                                        RESULT 12
US-09-563-222-142
; Sequence 142, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Heit, Mich B.
; TITLE OF INVENTION: EUKARYOTIC CELLS
; TITLE OF INVENTION: EUKARYOTIC CELLS
; TITLE REPRENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT PILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SEQ ID NO 142
; LENGTH: 30
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0; Indels
0; Mismatches
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25; Conservative
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ORGANISM: Homo sapien
US-09-563-222-142
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US-10-783-950-133
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RESULT 14 US-10-728-420B-91

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APPLICANT: WOULER, SUSAN L.
APPLICANT: WOLLER, SUSAN L.
APPLICANT: BURK, AIMEE
APPLICANT: BURK, AIMEE
TITLE OF INVENTION: ENGINEERED FAB' FRAGMENT ANTI-TUMOR
TITLE OF INVENTION: ANTI-RHEUMATIC DRUGS
FILLE REFERENCE: 12294-1010
CURRENT APPLICATION NUMBER: US/10/728,420B
CURRENT PILING DATE: 2003-12-05
PRIOR APPLICATION NUMBER: US 60/431,053
PRIOR APPLICATION NUMBER: US 60/431,053
PRIOR SEQ ID NOS: 117
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 91
LENGTH: 30
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US-10-728-420B-91
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100.0%; Score 120; DB 5;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 25; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 25; Conservative 0; Mismatches 0;
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Publication No. US20050042664A1
GARREAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: DamaChroder, Melisem
APPLICANT: Dall'Acqua, William
APPLICANT: Dall'Acqua, William
APPLICANT: Dall'Acqua, William
APPLICANT: DamaChroder, Melises
ATTLE OF INVERTION: HUMANIZATION OF ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT PILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SCOTWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 144
LENGTH: 30
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Sequence 91, Application US/10728420B Publication No. US20050042219A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-923-068-144
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April 25, 2006, 07:01:21 ; Search time 16.0377 Seconds (without alignments) 68.593 Million cell updates/sec
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2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

7: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

8: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	-268-33	-135	-590	-978	-886	-325	-325	-669	-669	-669	-669	-669	-554	-554	-554	-554	-846	-59(	-004-590-	-59(	-004-590-4	-59(	136-250-	-136-250-	-136-250-18
	11-105	-108	11-004-590-1	11-126-978-4	1-226-886-4	11-226-325-13	-226	-054	11-054-669-	-054	11-054-669-4	-054	1-084-554-	-084	11-084-554-	-084	1-061-848-	-004	-004	1-004-590-	-004	-004	1-136	-136	-136
	3-11	JS-11-108-135-4	3-11	38-11	US-11	<b>US-11</b>	3-11	JS-11-054-669-	<b>US-11</b>	JS-11-054-669-	US-11	JS-11-054-669-	US-11	JS-11-084-554-	US-11	US-11-084-554-2	US-11	US-11-004-590-	US-11	US-11	US-11	US-11-004-590-7		US-11	US-11
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23,	Sequence 50, Appl Sequence 51, Appl Sequence 52, Appl Sequence 56, Appl Sequence 87, Appl Sequence 84, Appl Sequence 86, Appl Sequence 86, Appl Sequence 86, Appl	111, 113, 126, 177, 86,
11-136-250 11-084-554 11-136-250	US-11-155-843-50 US-11-155-843-51 US-11-155-843-52 US-11-155-843-56 US-11-155-843-84 US-11-155-843-84 US-11-155-843-86	US-11-177-648-11 US-11-177-648-12 US-11-177-648-13 US-11-177-648-16 US-11-177-648-77 US-11-177-648-85
98 7 99 7 7	109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7 109 7	1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 1113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 113 7 1
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APPLICANT: Koenig, Scott
APPLICANT: Veri, Maria Concetta
APPLICANT: Veri, Maria Concetta
APPLICANT: Thaillon, Nadine
APPLICANT: Bonvini, Ezio
APPLICANT: Bonvini, Ezio
APPLICANT: Rankin, Christopher
TITLE OF INVENTION: Fc-gamma-RRIB-specific antibodies and methods of use thereof
TITLE REFERENCE: 11183-014-999
CURRENT APPLICATION NUMBER: US/11/108,135
CURRENT PILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/562,804
PRIOR FILING DATE: 2004-04-16
PRIOR PILING DATE: 2004-04-16
PRIOR PILING DATE: 2004-04-16
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US-11-105-268-33
US-11-105-268-33
Sequence 33, Application US/11105268
Sequence 33, Application US/11105268
Sequence 33, Application US/11105268
Sequence 33, Application US/0505026024A1
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-IL-9
TITLE OF INVENTION: ANTI-IL-9
TITLE OF INVENTION: ANTI-IL-9
CURRENT FILING DATE: 2005-04-12
CURRENT FILING DATE: 2005-04-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
LENGTH: 25
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100.0%; Score 120; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.5e-12;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Homo sapiens
US-11-105-268-33
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, OTHER INFORMATION: Framework sequence from human germline VH1-18 and JH6 - FR1
US-11-126-978-4
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Sequence 48, Application WJ11226886

Publication No. US20060057149A1

GENERAL INFORMATION:
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TITLE OF INVENTION: UTRUS AND THERREDIES AGAINST WEST THEREOF
TITLE OF INVENTION: UTRUS AND THERREDIES AGAINST WEST THEREOF
TITLE OF INVENTION: UTRUS AND THERREDIES AGAINST WEST THEREOF
THE REFERENCE: 11183-021-99
CURRENT FILING DATE: 2005-09-13

PRIOR FILING DATE: 2004-09-13

NUMBER OF SEQ ID NOS: 60

SEQ ID NO 48

LENGTH: 30
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Sequence 137, Application US/11226325
Sequence 137, Application US/11226325
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT TSUCHIYA, WASAVUKI
TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0274
CURRENT FAPLICATION NUMBER: US/11/226,325
CURRENT FILING DATE: 2005-09-15
FRIOR APPLICATION NUMBER: PCT/JP98/04469
FRIOR APPLICATION NUMBER: PCT/JP98/0469
FRIOR FILING DATE: 1998-10-02
FRIOR FILING DATE: 1998-10-03
FRIOR FILING DATE: 1998-10-03
FRIOR FILING DATE: 1998-10-03
FRIOR FILING DATE: 1998-10-03
FRIOR FILING DATE: 1908-10-03
FRIOR FILING DATE: 1908-10-03
FRIOR FILING DATE: 1908-10-03
FRIOR FILING DATE: 1907-10-03
      PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: 60/569,882
PRIOR FILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASICSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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ORGANISM: homo sapiens
FRATURE:
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ORGANISM: Homo sapiens
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| Sequence 111. Application No. US2006000883A1
| GENERAL INFORMATION:
| APPLICANT: Lazar, Gregory Alan
| APPLICANT: Lazar, Gregory Alan
| APPLICANT: Lazar, Gregory Alan
| APPLICANT: Hammond, Phillib W.
| TITLE OF INVENTION: WETHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
| TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
| TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
| FILE REPERENCE: 185832/US/5
| CURRENT APPLICATION NUMBER: US 60/527,167
| PRIOR PPLING DATE: 2004-06-21
| PRIOR PPLING DATE: 2004-06-21
| PRIOR PPLING DATE: 2004-06-13
| PRIOR PPLING DATE: 2004-08-13
| PRIOR PLING DATE: 2004-10-14
| NUMBER OF SEQ ID NOS: 458
| SEQ ID NO 111
| LENGTH: 30
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Publication No. US20060013810A1
GENERAL INFORMATION:
APPLICANT: Johnson, Leslie Sydnor
APPLICANT: Huang, Ling
TITLE OF INVENTION: HUMANIZED FCGammaRIIB-SPECIFIC ANTIBODIES AND METHODS OF USE THER
FILE REFERENCE: 11183-018-999
CURRENT APPLICATION NUMBER: US/11/126,978
CURRENT FILING DATE: 2005-05-10
PRIOR APPLICATION NUMBER: 60/582,043
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US-11-108-135-4
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PRIOR APPLICATION NUMBER: US 60/582,045
PRIOR FILING DATE: 2004-06-21
PRIOR PILICATION NUMBER: US 60/654,713
PRIOR FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PREFSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 30
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Matches 25, Conservative
                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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US-11-004-590-111
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; ORGANISM: Homo sapiens
US-11-054-669-1
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Amino acid CTHER INFORMATION: sequence of the H chain V region (1) HG3 US-11-226-325-137
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100.0%; Score 120; DB 7; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
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; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICATION:
; APPLICATION:
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILER REFERENCE: 30219/US/3;
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US/11/054,669
; PRIOR APPLICATION NUMBER: US/11/054,669
; PRIOR PILING DATE: 2002-07-12
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin version 3.3
; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0274
CURRENT APPLICATION NUMBER: US/11/226,325
CURRENT FILING DATE: 2005-09-15
PRIOR APPLICATION NUMBER: US/09/509,098
PRIOR PILING DATE: 1990-03-22
PRIOR PILING DATE: 1990-10-02
PRIOR PILING DATE: 1997-10-03
PRIOR PILING DATE: 1997-10-03
PRIOR PILING DATE: 1997-10-03
PRIOR PILING DATE: 1997-10-03
SOFTWARE: PALENTING VET: 2.1
SEQ ID NO 200
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ORGANISM: Artificial Sequence
                                                         TYPE: PRT ORGANISM: Artificial Sequence
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           SEQ ID NO 137
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100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
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Query Match 100.0%; Score 120; DB 7; Length 98; Best Local Similarity 100.0%; Pred. No. 3.7e-11; Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                       Sequence 2, Application US/11054669
; Sequence 2, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
   APPLICANT: Foote, Jefferson
; TILLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2002-07-12
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2.
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TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILLE REFERENCE: 30219/US/3
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT PILING DATE: 2005-02-09
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOPTWARE: PATENTIN VETSION 3.3
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Sequence 16, Application US/11084554

Publication No. US2005026679A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kellermann, Sirid-Ai
APPLICANT: Korver, Wouter
TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
FILE REFERENCE: ABGENIX.100A
CURRENT PELING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: 60/554,372
PRIOR APPLICATION NUMBER: 60/554,372
PRIOR APPLICATION NUMBER: 60/554,372
PRIOR FILING DATE: 2004-03-19
PRIOR FILING DATE: 2004-06-24
NUMBER OF SEQ ID NOS: 266
SOFTWARE: PASESEG for Windows Version 4.0
SEQ ID NO 16
INDIREMENTION OF THE PASE OF T
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Publication No. US2005026679A1
GENERAL INFORMATION:
APPLICANT: Kellermann, Sirid-Ai
APPLICANT: Kellermann, Sirid-Ai
APPLICANT: Korver, Wouter;
TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN;
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION;
TITLE OF INVENTION: ANTIBODIES 2005-03-17
CURRENT APPLICATION NUMBER: US/11/084,554
CURRENT FILING DATE: 2005-03-17
PRIOR PILING DATE: 2004-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 120; DB 7; Length 98; Best Local Similarity 100.0%; Pred. No. 3.7e-11; Matches 25; Conservative 0; Mismatches 0: Tadala
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100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/11/084,554
CURRENT FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: 60/554,372
PRIOR PILING DATE: 2004-03-19
PRIOR PILING DATE: 2004-03-19
PRIOR PILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 266
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 98
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Sequence 15, Application US/11084554
PUBLICATION NO. US20050260679A1
GENERAL INFORMATION:
APPLICANT: Kellermann, Sirid-Ai
APPLICANT: Green, Larry L.
APPLICANT: Korver, Wouter
TITLE OF INVENTION: REDUCTING THE RISK OF HUMAN ANTI-HUMAN
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
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Publication No. US20050261480A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/US/3;
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT APPLICATION NUMBER: US 10/194,975
FRIOR APPLICATION NUMBER: US 60/305,111
FRIOR APPLICATION NUMBER: US 60/305,111
FRIOR APPLICATION NUMBER: US 60/305,111
FRIOR FILING DATE: 2002-07-12
NUMBER: OF SEQ ID NOS: 124
SOFTWARE: PATENTIN VERSION 3.3
                                                                                                                                                                                    JABEACH INFORMATION: SUPER HUMANIZED ANTIBODIES
TILLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 3013/9(3)
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
PRIOR PILING DATE: 2005-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin version 3.3
SEQ ID NO 4
LENGTH: 98
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                                                                            ; Sequence 4, Application US/11054669; Publication No. US20050261480A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Matches 25; Conserv
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US-11-054-669-7
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prior Application NUMBER: 60/574,661

prior Filing Date: 2004-05-24

NUMBER OF SEQ ID NOS: 266

SOTTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 98

TYPE: PRT

ORGANISM: Homo sapiens

US-11-084-554-18

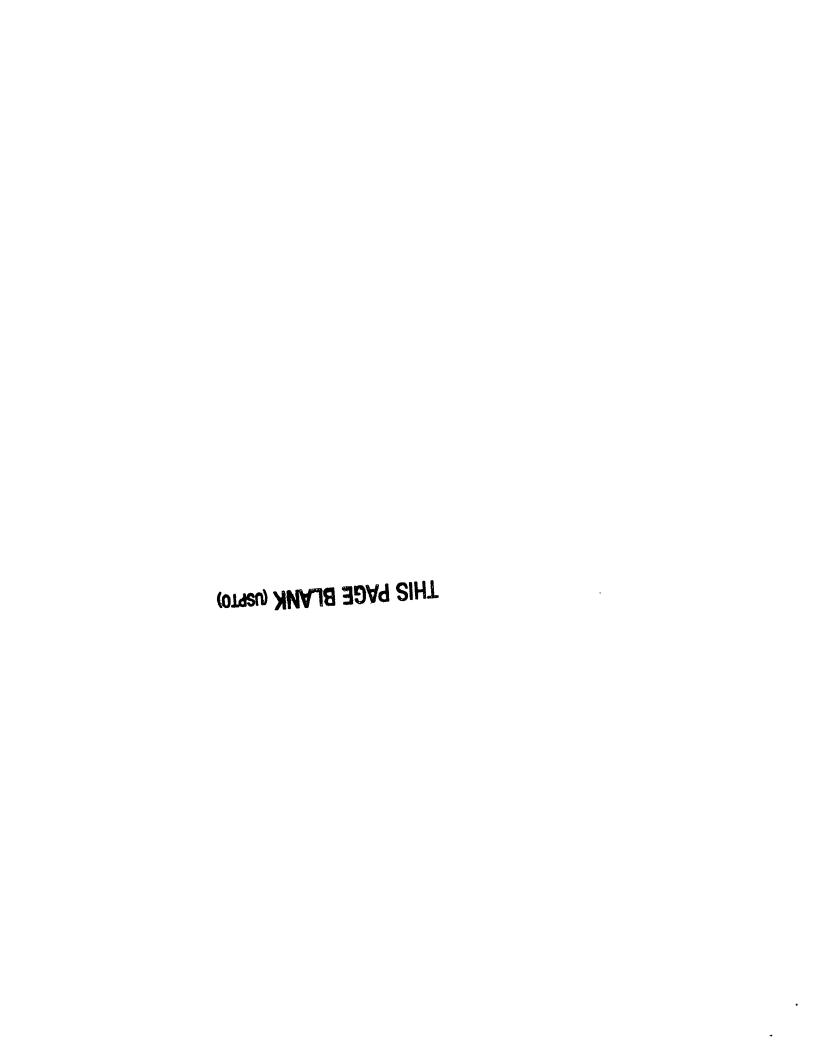
Query Match
Best Local Similarity 100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
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0; Gaps

Search completed: April 25, 2006, 07:10:01 Job time : 16.2044 secs

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April 25, 2006, 06:05:16; Search time 133.491 Seconds (without alignments) 82.286 Million cell updates/sec
GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003as:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Adg90698 Anti-VEGF Ady31549 Human ant Abg98300 Human ant Abg98301 Human ant Ady31417 Human ant Aea21493 Human ant Aea21493 Human ant Aea29829 Anti-MUC1 Adg99849 Anti-MUC1 Adg99849 Anti-MUC1 Adg99849 Anti-MUC1 Adg99849 Anti-MUC1 Adg99849 Anti-MUC1 Adg9984 Anti-MUC1 Adg9984 Anti-MUC1 Adg9984 Anti-MUC1 Adg9984 Anti-MUC1 Adg9984 Anti-MUC1 Adg9980 Human ger Abc27105 Human ger Abc27105 Human ger Adc99846 Germline Adc99846 Germline Adc99846 Germline Description SUMMARIES ARA21493 ARA21457 ADC99829 ADD05433 ADF09871 ADC99849 ADC99844 ADC99836 ADC99816 ADY31417 ABG78215 ABG91906 ADQ90698 AAU70466 ADF09891 ADC99817 8 Query Match Length 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.0 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 11124 Result Š

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### ALIGNMENTS

RESULT 1 ADQ90698

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Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 21:*

Датараве :

antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antinflammatory; antianglogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; angiogenic disorder; immunological disorder; anti-VEGF antibody; anti vascular endothèlial cell growth factor antibody; heavy chain; FR1. Anti-VEGF antibody heavy chain FR1 subgroup II peptide SEQ ID NO:2. ADQ90698 standard; peptide; 25 AA. 23-JAN-2004; 2004WO-US001844 23-JAN-2003; 2003US-0442484P. (first entry) (GETH ) GENENTECH INC. WO2004065417-A2. Homo sapiens. Synthetic. 05-AUG-2004. 21-0CT-2004 ADQ90698; 

Simmons L;

WPI; 2004-562149/54.

Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.

Claim 15; SEQ ID NO 2; 161pp; English.

The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid

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the amino acid found at the corresponding FR position of a human subgroup variable domain consensus sequence that has a hypervariable region 1 (HVR1) and/or HVR2 amino acid sequence with the most sequence identity with a corresponding HVR1 and/or HVR2 sequence of the variable domain.

The antibody or antigen binding fragment variable domain comprises the modified R that has improved Yield in cell culture compared to an unmodified antibody or antigen-binding fragment. The antibody and antigen binding fragment The antibody and antigen binding fragment and in antibody series.

The inding fragment have cytostatic, antinflammatory, antiangiogenic and immunomodulatory activities, and can be used in antibody therapy. The methods and compositions of the present invention are useful for producing antibodies or antigen binding fragments in cell culture, in particular for improving the yield of recombinant antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and infundological disorders. The present candothelial cell growth factor) antibody, which is used in the cadenar antibody can antibody, which is used in the cempular candothelial cell growth factor) antibody, which is used in the
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where the different amino acid is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 124; DB 8;
Pred. No. 5.8e-10;
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position with a different amino acid,
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13-OCT-2003; 2003US-0510741P.
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 AA;
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The invention relates to an antibody which binds to an epitope on gp39, is new, where the epitope is distinct from the epitope bound by IDEC-131, and the antibody has a non-agonistic effect on T-cell activation and inhibits gp39/CD40 interaction. Also included are: (1) an improved method inhibits gp39/CD40 interaction comprishing administering an antibody specific for gp39/CD40 interaction comprishing administering an antibody interaction comprishing an antibody specific for gp39 that inhibits the gp39/CD40 interaction and is non-agonises B-cell differentiation and antibody production, and is non-agonises B-cell differentiation and antibody production, and is non-agonistic of T-cell activation; (3) a DNA sequence which encodes an antibody edined above; (4) an expression vector, which conclains a DNA sequence of (3); (5) a method of suppressing vector, which conclains a DNA sequence of (3); (5) a method of suppressing control and/or cellular immune responses against cells or vectors administering or after gene therapy comprising further administering prior, during or after gene therapy comprising further administering collular interaction of cells, tissues or organs of the same or different species into a subject, where the improvement comprises administering an antibody defined above prior, during or after transplantation, to suppress immune responses gapainst the transplanted cell; tissue or organ against the responses elicited by the transplanted cell, tissue or organ against the responses host. The antibody is useful for preventing graft rejection, and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody; variable region; light chain; heavy chain; VH; VL; gp39; CD40; T-cell activation; B-cell differentiation; framework region; cellular immune response; gene therapy; graft rejection; human; FR; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes; asthms; multiple sclerosis; allergy; diabetee mellitus; systemic lupus erythematosus; graft-versus-host disease.
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                                                        Length 25;
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                                                        100.0%; Score 124; DB 9;
100.0%; Pred. No. 5.8e-10;
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                                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVS
                                                                                                                                                                                                                                                                                                     ABG98300 standard; peptide; 30 AA
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                                                                             Local Similarity 100.
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                  Sequence 25 AA;
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Matches
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for

antibody from a first species for use in a second species. The presen amino acid sequence represents a human germline heavy chain framework

peptide

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treating autoimmune diseases, e.g., rheumatoid arthritis, multiple sclerosis, diabetes, asthma, multiple sclerosis, allergic conditions, diabetes mellitus, or systemic lupus erythematosus, as well as non-autoimmune diseases such as graft-versus-host disease (many other diseases and conditions are given in the specification). The antibodies are also useful in gene or cellular therapy, and to inhibit humoral and cellular immune responses against viral vectors. The present sequence is a framework region (FR) fragment of a human anti-gp39 antibody used to determine which amino acids should be humanised in a mouse anti-gp39
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Sequence 30 AA;

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Length 30;
                          Indels
100.0%; Score 124; DB 5;
100.0%; Pred. No. 6.9e-10;
ive 0; Mismatches 0;
                                                                       1 QVQLQBSGPGLVKPSQTLSLTCTVS 25
                                                       1 QVQLQESGPGLVKPSQTLSLTCTVS 25
                            25; Conservative
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Gaps

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ABG98301 standard; peptide; 30 AA. ABG98301

ABG98301;

08-JAN-2003 (first entry)

Human antibody 3d75d germline kappa chain variable region FR1.

Antibody; variable region; light chain; heavy chain; VH; VL; gp39; CD40; T-cell activation; B-cell differentiation; framework region; cellular immune response; gene theorapy; graft rejection; human; FR; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes; sasthma; multiple sclerosis; allergy; diabetes mellitus; systemic lupus erythematosus; graft-versus-host disease. 

Homo sapiens.

WO200194586-A2

13-DEC-2001.

06-JUN-2001; 2001WO-US018098

06-JUN-2000; 2000US-0209584P

(IDEC-) IDEC PHARM CORP.

Rastetter WH, Kloetzer WS; Hanna N, Anderson DR, Pan LZ,

New antibodies binding to an epitope on gp39, useful for preventing graft rejection, or for treating autoimmune diseases (e.g. diabetes, asthma or multiple sclerosis), and non-autoimmune diseases (e.g. graft-versus-host WPI; 2002-188261/24. disease).

Disclosure; Page 47; 130pp; English.

The invention relates to an antibody which binds to an epitope on gp39, is new, where the epitope is distinct from the epitope bound by IDEC-131, and the antibody has a non-agonistic effect on T-cell activation and inhibits gp39/CD40 interaction. Also included are: (1) an improved method of treating a disease by modulating gp39 expression or inhibiting the gp39/CD40 interaction comprising administering an antibody specific for gp39 that inhibits the gp39/CD40 interaction and is non-agonistic of T-cell activation; (2) an antibody which antagonises B-cell differentiation and antibody production, and is non-agonistic of T-cell activation; (3) a bNA sequence which encodes an antibody defined above; (4) an expression vector, which contains a DNA sequence of (3); (5) a method of suppressing

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continuous analysis remains the continuous continuo continuo
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humoral and/or cellular immune responses against cells or vectors
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with polypeptides in transfected cells, to generate an IgBP that binds to a rigand, and transferned plant cells, to generate an IgBP that binds to arigand, and transformed plant cells are selected, and preparing an IgBP array in plant cells. At least one peptide sequence has at least 75# sequence identity to a framework region (PR) of a native IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (GRBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammallan cells). The CHBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an
                                                                                                                                                                                                                                                  derived peptide that may be incorporated into an IgBP of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ody from a first species for use in a second species. The present acid sequence represents a human germline heavy chain framework
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                                                                                                                                                                                                                                                                                                                                ch 100.0%; Score 124; DB 5; Length 30; Similarity 100.0%; Pred. No. 6.9e-10; 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human antibody heavy chain framework peptide - SEQ ID 249.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADY31417 standard; peptide; 30 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-180802/19
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Best Local Similarity
Matches 25; Conserv
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This invention relates to a novel isolated human antibody that specifically binds to secretory leukocyte protease inhibitor (SLPI). The invention may be useful for the development of compounds with a cytostatic activity or for immunotherapy. The antibody, composition and methods are useful for treating and preventing cancer. The antibodies are useful for the presence of SLPI in biological samples. The present sequence is that of a peptide which was used during the development of the novel antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human antibody that specifically binds to secretory leukocyte protease inhibitor \{SLPI\}, useful for treating and preventing
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                                                                                                                                                                                                                                                                                                                                                                                       Zhong H;
                                                                                                                                                                 Human anti-SLPI antibody-related peptide SegID57.
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                                                                                AEA21493 standard; peptide; 30 AA
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Matches 25; Conserv
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New human anti-MUC18 monoclonal antibodies, useful for treating a disease
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hes 25; Conservative
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                       WO2005047328-A2.
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The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has
                                                                                                    The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to WUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of WUC18 on the cell surface such as tumours, specifically melanoma, oseophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraspithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human WUC18 antibody-related consensus protein of the invention derived from analysis of germline gene region proteins and anti-human WUC18 monoclonal antibody sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 124; DB 7;
100.0%; Pred. No. 2.2e-09;
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Best Local Similarity 100.
Matches 25; Conservative
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                                                                            Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel isolated human antibody that specifically binds to secretory leukocyte protease inhibitor (SLPI). The invention may be useful for the development of compounds with a cytostatic activity or for immunotherapy. The antibody, composition and methods are useful for treating and preventing cancer. The antibodies are useful for detecting the presence of SLPI in biological samples. The present sequence is that of a peptide which was used during the development of the novel antibody of the invention.
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                                                                                                                                                                                                                                                                                                                                                       New isolated human antibody that specifically binds to secretory leukocyte protease inhibitor (SLPI), useful for treating and preventing
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cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-MUC18 monoclonal antibody-related consensus protein #9
                                                                                                                                                                                                                                                                                                                                                             Length 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                       ilarity 100.0%; Score 124; DB 7; ilarity 100.0%; Pred. No. 2.2e-09; Conservative 0; Mismatches of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                                                                                                                                                                                     consensus protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSQTLSLTCTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP09871 standard; protein; 95 AA
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Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-598367/56.
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                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                           Sequence 95 AA;
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ADFO98
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invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, osophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 antibody-related consensus protein of the invention derived from analysis of germline gene region proteins and anti-human MUC18 monoclonal antibody sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-human MUC18 antibody-related consensus protein SEQ ID 78.
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100.0%; Pred. No. 2.2e-09;
iive 0; Mismatches 0;
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                               QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                                                                                                                                    ADC99849 standard; protein; 98
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nes 25; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lung cancer.
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IID ADC9

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Gaps

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The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises cumour growth in an animal. The tumour inhibition process comprises comprises can animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in thibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumourse, inhibiting cumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region,
                         Anti-MUC18 antibody heavy chain variable region V4-31 consensus protein.
                                                                                                       monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2001; 2001US-0346460P.
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Length 98;
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Anti-MUC18 monoclonal antibody-related consensus protein #19
                       (first entry)
                       12-PBB-2004
          ADF09891
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Lazarovits J, , Peretz T; Plaksin D, Hagai Y, cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; consensus.

WO2003057837-A2.

Synthetic.

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The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastaais. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other melignancies. The present amino acid sequence is a consensus sequence from an alignment between an MUC18 tumour antigen-specific monoclonal antibody of the invention and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, Fv molecule, hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                       Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 124; DB 7; Best Local Similarity 100.0%; Pred. No. 2.2e-09; Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 78; 83pp; English.
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                                                                       28-DEC-2001; 2001US-0346414P.
                                         26-DEC-2002; 2002WO-US041580
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                                                                                                                                                              WPI; 2003-598367/56
                                                                                                     (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                           related protein.
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Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other cella.

Claim 13; Page 194-195; 232pp; English

The invention relates to a peptide or polypeptide comprising an Fy molecule, a construct or fragments or a construct of a fragment with chanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is cancered binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is chain FV (scPV) or a disulfide FV (dsFV). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and medianoma, where the leukaemia cell is an composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human FV molecule hypervariable region related peptide of the invention

Sequence 99 AA;

Gaps ö Length 99; Query Match 100.0%; Score 124; DB 5; Length 9 Best Local Similarity 100.0%; Pred. No. 2.3e-09; Matches 25; Conservative 0; Mismatches 0; Indels

.; 0

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Search completed: April 25, 2006, 06:15:10 Job time : 134.491 secs

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April 25, 2006, 06:25:05; Search time 33.7264 Seconds (without alignments) 61.284 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                     US-10-764-428-2
124
1 QVQLQBSGPGLVKPSQTLSLTCTVS 25
                                                                                                                                                                                                                                                                                                                                            572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                sw model
                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                              - protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                     OM protein
                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Issued Patents AA:*

1. /cgn2 6/ptodata/1/iaa/5_COMB.pep:*

2. /cgn2 6/ptodata/1/iaa/6_COMB.pep:*

3. /cgn2 6/ptodata/1/iaa/H_COMB.pep:*

4. /cgn2 6/ptodata/1/iaa/H_COMB.pep:*

5. /cgn2 6/ptodata/1/iaa/RE COMB.pep:*

7. /cgn2 6/ptodata/1/iaa/RE COMB.pep:*

8. /cgn2 6/ptodata/1/iaa/RE COMB.pep:*

Database :

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# SUMMARIES

	, App							Appl	Appl	Appl				Appl	Appl	Appl	Appl	Appl	Appli	Appl	, App	, App	Appli	Appli	Appli	Appli	Appli
្ត <u> </u>	137	13,	20,	13	20,	13,	20,	58,	78,	36,	38,	39,	45,	46,		65,		77,		13	116	116	'n	'n	'n	'n	Ŋ
Description	Sequence	Sequence				Sequence	Sequence	Sequence	Seguence	Sequence				Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence
ID	US-09-563-222C-137	US-08-554-840-19	US-08-554-840-20	US-08-925-339-19	US-08-925-339-20	US-09-332-595-19	US-09-332-595-20	US-10-330-613A-58	US-10-330-613A-78	US-10-194-975-36	US-10-194-975-38	US-10-194-975-39	US-10-330-613A-45	US-10-330-613A-46	US-10-330-613A-57	US-10-330-613A-65	US-10-330-613A-73	US-10-330-613A-77	US-10-330-613A-5	US-10-330-613A-13	US-08-545-809A-116	US-09-515-697-116	US-08-360-125-5	US-08-450-578-5	US-09-017-628-5	US-09-014-880-5	US-08-450-363-5
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* Query Match Length	30	87	87	87	87	87	87	95	98	66	66	66	66	66	66	66	66	66	117	117	118	118	119	119	119	119	119
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124
Result No.		0	M	4	· LC	9	7	· 00	ð	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

Sequence 5, Appli Sequence 25, Appl Sequence 838, App	Sequence 128, App Sequence 135, App Sequence 128, App	21,	Sequence 21, Appl Sequence 21, Appl	16,	Sequence 10, Appl Sequence 70, Appl Sequence 42, Appl	Sequence 50, Appl Sequence 42, Appl	Sequence 51, Appl
US-09-467-903-5 US-10-330-613A-25 US-09-471-276-838	US-08-137-117D-128 US-08-137-117D-135 US-08-436-717-128	US-08-436-717-135 US-08-554-840-21	US-08-925-339-21 US-09-332-595-21	US-08-554-840-16 US-08-925-339-16	US-09-332-595-16 US-10-330-613A-70		US-10-194-975-51
119 2 119 2 136 2	1000	30 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	76 2 76 2	87 2	94 2 2 2	96 20 20 20 20 20 20 20 20 20 20 20 20 20	97 23
100.0	97.6	97.6	97.6		997.		97.6
124	121	1212	121	121	121	121	121
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	322	3 3 4 S	36 37	38 39	6 4 4 6 4 6	4 4 4	4 4 5

### ALIGNMENTS

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RESULT 2
US-08-554-840-19
US-08-554-840-19
Sequence 19, Application US/08554840
Fatent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: HANNA, Nabil
APPLICANT: BALLAN Eduard A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: Burna, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
Sequence 137, Application US/0956322C

Sequence 137, Application US/0956322C

Batent No. 6696620

GENERAL INFORMATION:
APPLICANT: BICTYE PHARMACEUTICALS, INC.
APPLICANT: HIATY, ANDREW C.
TITLE OF INVENTION: INMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REFERENCE: 068904-0501
CURRENT PELLICATION NUMBER: US/09/563,222C
CURRENT PELLICATION NUMBER: US/09/563,222C
PRIOR APPLICATION NUMBER: 09/563,222
FRIOR APPLICATION NUMBER: 09/563,222
FRIOR APPLICATION NUMBER: 09/563,222
FRIOR PILLING DATE: 2000-05-02
FRIOR PILLING DATE: 2000-05-02

NUMBER OF SEQ ID NOS: 182

SOFTWARE PATENT NOS: 182
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Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 25; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
US-09-563-222C-137
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                                                                                                                         Query Match 100.0%; Score 124; DB 2; Length 87; Best Local Similarity 100.0%; Pred. No. 7.7e-12; Matches 25; Conservative 0; Mismatches 0; Indels
1 QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                                                                                                                    1 OVOLOESGPGLVKPSQTLSLTCTVS 25
                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                US-08-554-840-19
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US-08-554-840-20
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US-GR-925-339-19

US-GR-925-339-19

SEQUENCE 19, Application US/08925339

Patent No. 6440418

GENERAL INFORMATION:
PAPLICANT: BLACK, Amelia

APPLICANT: BADLAN, Reduard A.

TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,

TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,

TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSES: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STRATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER: IBM PC COMPAILIBE

COMPUTER: IBM PC COMPAILIBE

COMPUTER: IBM PC COMPAILIBE

SOFTWARE: PLODS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/925,339
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CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
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                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSQTLSLTCTVS 25
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 87 amino acids
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                                                                                            , MOLECULE TYPE: protein US-08-554-840-20
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STRANDEDNESS: si
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Best Local Similarity 100. Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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MOLECULE TYPE: protein
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22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino a
STRANDEDNESS:
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US-09-332-595-20
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; SQUENCE 19, Application US/09332595
; Patent No. 6506383
; GENERAL INFORMATION:
; PAPLICANT: BLACK, Amelia
; APPLICANT: BLACK, Amelia
; APPLICANT: PADLAN, Roland A.
; APPLICANT: PREMAN, Roland A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEB: Burns, Doane, Swecker & Mathis
; CITY: Alexandria
; CITY: Alexandria
; STATE: Virginia
; STATE: Virginia
; STATE: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                  APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: HANNA, Nabil
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
TITLE OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
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                                                                                                                                                                                                                                                                                                  COUNTRY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 124; DB 2;
100.0%; Pred. No. 7.7e-12;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
ATTORNEY/AGENT INPORMATION:
                    Sequence 20, Application US/08925339
Patent No. 6440418
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REPERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 25; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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US-09-332-595-19
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           US-08-925-339-20
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COMPUTER: IN Flory disk
COMPUTER: IN FORM:
COMPUTER:
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QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                                                                                                                                                      Length 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUCIB ANTIGEN
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUCIB ANTIGEN
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUCIB ANTIGEN
TITLE OF INVENTION: ADSCRIZE . 2021.
CURRENT APPLICATION NUMBER: 60/346299
FRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 78
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUCIS ANTIGEN
FILLE REPERENCE: ABGENIX. 022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                   Score 124; DB 2;
Pred. No. 7.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 124; DB 2;
Best Local Similarity 100.0%; Pred. No. 8.5e-12;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                0; Mismatches
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Patent No. 6924360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-330-613A-58
; Sequence 58, Application US/10330613A
; Patent No. 6924360
TELECOMMUNICATION INFORMATION:
        TELEPHONE: (703) 836-6620
TELEPAX: (703) 816-2021
INPORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 aming acids
                                                                                                                                                                                                                                                   Query Match

Best Local Similarity 100.0%;

Matches 25; Conservative 0
                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-332-595-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-10-330-613A-78
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ORGANISM: Homo sapiens
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LENGTH: 95
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Gaps

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                                                                                  US-10-194-975-36

Sequence 36, Application US/10194975

Patent No. 6881557

GENERAL INFORMATION:

TITLE OF INVENTION: Super Humanized Antibodies

PILE REFRENCE: 501231.01

CURRENT APPLICATION NUMBER: US/10/194,975

CURRENT PILING DATE: 2002-10-10

PRIOR REPLICATION NUMBER: US 60/305,111

PRIOR PILING DATE: 2001-07-12

PRIOR FILING DATE: 2001-07-12

NUMBER: OF SEQ ID NOS: 122

SOFTWARE: PatentIn version 3.1

SEQ ID NO 36

IRNGTH 036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FOOLE, Jefferson
TILLE OF INVENTION: Super Humanized Antibodies
TITLE OF INVENTION: Super Humanized Antibodies
TITLE OF INVENTION: Super Humanized Antibodies
TITLE OF INVENTION: Super Humanized Antibodies
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILLED APPLICATION NUMBER: US 60/305,111
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILLE APPLICATION NUMBER: US 60/305,111
SOFTWARE: PatentIn version 3.1
SEQ ID NO 38
LENGTH: 99
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Patent No. 6881557
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231 01
CURRENT APPLICATION NUMBER: US/10/194,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGFGLVKPSQTLSLTCTVS 25
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1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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US-10-144-975-38
Sequence 38, Application US/10194975
; Patent No. 6881557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
COCCANISM: Homo sapiens
US-10-194-975-38
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ORGANISM: Homo sapiens
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Best Local Similarity
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100.0%; Score 124; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0; Indels
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US-10-330-613A-46

US-10-330-613A-46

Sequence 46, Application US/10330613A

Patent No. 6924360

GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF UNENTION: ANTIBODIES AGAINST THE WUC18 ANTIGEN
TITLE REPERENCE: ABGRAIX.022A

CURRENT APPLICATION NUMBER: US/10/330,613A

CURRENT PILING DATE: 2002-12-26

PRIOR PILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 90

SOFTWARE: PRECED FOR Windows Version 4.0

SEQ ID NO 46

LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-10-330-613A-45
; Sequence 45, Application US/10330613A
; Batent No. 6924360
; GENERAL INFORMATION:
    APPLICANT Gudas, Jan
    TITLE OUGHS, ANTIBODIES AGAINST THE MUC18 ANTIGEN
    TITLE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT APPLICATION NUMBER: 60/346299
PRIOR PILING DATE: 2001-12-18
; WINDER OF SEQ ID NOS: 90
; SOFTWARE: PASESEG for Windows Version 4.0
; SEQ ID NO 45
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Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSQTLSLTCTV8 25
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 39
LENGTH: 99
                                                                                                                                                                                                                                                                                                1 QVQLQBSGPGLVKPSQTLSLTCTVS 25
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US-10-330-613A-45
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                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-10-194-975-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-330-613A-46
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0y 1 0VOLOESGPGIVKESGTISITCTVS 25

RESULT 15

US-10-330-613A-57

Sequence 57, Application US/10330613A
Patent No. 6924360

GENERAL INFORMATION:
PAPELICANT: Gudas, Jean
TITLE OF INVERTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX.022A

CURRENT FILING DATE: 2002-12-26

PRIOR PELING DATE: 2001-12-18

FRIOR FILING DATE: 2001-12-18

SOSTWARE: FastSEQ for Windows Version 4.0

SOSTWARE: FAST OF MURCHEN CONSTRUCTORS: SEQ ID NO 57

LENGTH: 99

TYPE: PT

CONGANISM: Homo sapiens
US-10-330-613A-57

QUECNEY MARCH

US-10-330-613A-57

QUECNEY MARCH

UQULOESGPGIVKPSQTLSITCTVS 25

DD 1 QVOLOESGPGIVKPSQTLSITCTVS 25

DD 1 QVOLOESGPGIVKPSQTLSITCTVS 25

DD 1 QVOLOESGPGIVKPSQTLSITCTVS 25

Search completed: April 25, 2006, 06:28:41
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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sw model - protein search, using OM protein

April 25, 2006, 06:15:41; Search time 21.2264 Seconds (without alignments) 113.322 Million cell updates/sec

Run on:

US-10-764-428-2 124 1 QVQLQBSGPGLVKPSQTLSLTCTVS 25

score: Title: Perfect

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

PIR 80:* Database :

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	g heavy		g heavy c	lambda chain	g heavy	heavy	g heavy	g heavy	g heavy	heavy	heavy	heavy	heavy	heavy		heavy	g heavy cha		potheti	Ig heavy chain - h	heavy	-	Ig heavy chain V r						
	ΩÏ	S26801	S26803	830534	S31585	526804	S26906	PH0876	\$12421	826807	S44125	S57464	B26340	S18557	S20780	A26340	S44113	830530	S31514	831690	831673	831676	831696	831586	137782	A24770	831512	831511	$\sim$	S26802
	80	2	7	~	~	~	~	~	~	~	~	~	~	~	~	7	~	7	~	7	7	~	7	7	~	~	~	~	N	N
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Ig heavy chain pre Ig heavy chain V r Ig heavy chain V r	chain in pre chain chain	mu heavy comunity com	Ig mu heavy chain Ig mu heavy chain Ig heavy chain V r Ig heavy chain V r
E34964 S12412 S12418	S78056 PT0370 S31684 S31604	S78051 S54225 S54231 S54248 S54248	S54226 S54232 S09711 S13519
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111 99 99	120 120 135 135	135 138 140 141	141 142 146
96.0 95.2	99999	999999	955.2
119	118	118 118 118	118 118 118
30 31	3 3 3 3 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	37 38 44 41	4 4 4 4 (4 6 4 10

### ALIGNMENTS

Jaheavy chain V region (DP-65) - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000

C;Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000

C;Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000

C;Date: 13-Jan-1995 #sequence_revision 25-000

R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.

Bur. J. Immunol. 22, 1075-1082, 1992

A;Title: Polymorphism of human jmmunoglobulin V(H) 4 germ-line genes.

A;Residues: Sz6801

A;Status: preliminary

A;Residues: DA

A;Residues: 1-99 *WEN>

A;Residues: 1-99 *WEN>

A;Residues: 1-99 *WEN>

A;Residues: 1-99 *WEN>

A;Tomlinary

A;Residues: 1-99 *WEN>

A;Tomlinary

A;Residues: 1-90 *WEN>

A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A;Reference number: 826885; MUID:93021117; PMID:1404388

A; Accession: S26900

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-99 <TOM>

A.Cross-references: UNIPARC:UP10000116419; EMBL:Z12365; NID:g12948; PIDN:CAA78235.1; PIC C;Superfamily: immunoglobulin V region; immunoglobulin Nomology C;Keywords: heterotetramer; immunoglobulin P;15-99/Domain: immunoglobulin homology <IMM>

Gaps ö Query Match
100.0%; Score 124; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.8e-12;
Matches 25; Conservative 0; Mismatches 0; Indels

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## OVOLORSGPGLVKPSQTLSLTCTVS 25 δ 셤

RESULT 2

Jakeavy chain V region - human C;Species: Homo sapiens (man) C;Accession: 32-500 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000 C;Accession: S26803 J. Vu-Lee, L.; Marcus, D.M. R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M. Eur. J. Immunol. 22, 1075-1082, 1992 A;Atitles: Polymorphism of human immunoglobulin V(H) 4 germ-line genes. A;Reference number: S26803 A;Accession: S26803 A;Accession: S26803 A;Accession: S26803 A;Accession: Lype: DNA A;Accession: S26803 A;Accession: S26803 A;Accession: S26803 A;Accession: S26803 A;Coss-references: UNIPARC:UPI0000116485; EMBL:Z14238; NID:G37710; PIDN:CAA78607.1; PI

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A;Cross-references: UNIPARC:UPI00004CF85; EMBL:Z14240; NID:g37712; PIDN:CAA78609.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-97 < TOM>
A; Roces = cesignated DP-71
R; Sanz, 1:; Kelly, P:; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
Rsho J. 8, 3741-3748, 199 (H) gene families display remarkably little polymorphism.
A; Title: The smaller human V(H) gene families display remarkably little polymorphism.
A; Reference number: S09421; MUID:90059975; PMID:2511001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region (DP-71 / VH 4.11 / 4.15) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26906; S09421; S12415
C;Accession: S26906; S09421; S12415
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
Myrithe: The repertoire of human germline V(H) sequences reveals about fifty groups of 'A;Reference number: S26885; MUID:93021117; PMID:1404388
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C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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C;Accession: S26804
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Pulmorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26804
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
97.6%; Score 121; DB 2; Length 97;
Best Local Similarity 96.0%; Pred. No. 1.9e-11;
Matches 24; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 97;
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Pred. No. 1.9e-11;
1; Mismatches 0;
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Best Local Similarity 96.0%;
Matches 24; Conservative
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A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-97 <8A2>
                                                                                                                                                                                                                                                                                             A; Molecule type: DNA A; Residues: 1-97 < WEN>
                                                                                                                                                                                                                                                             A;Status: preliminary
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A;Accession: S31585
A;Status: preliminary
A;Aclocule type: mCNI
A;Moldcule type: mCNI
A;Rosidus: 1-137 cCNI>
A;Cross-references: UNIPARC;UPI000011646C; EMBL:Z14193; NID:g30973; PIDN:CAA78562.1; PID
C;Superfermily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;34-117/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 831885
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
B;Dubnitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: 831585
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530534
Globaly chain V region - human
Globale: New Sapiens (man)
Clobate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
Clobate: 07-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
Clobate: 08-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
Clobate of Sapient Sa
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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                                                                                                                                                                            Length 99;
                        C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
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A;Cross-references: UNIPARC;UPI0000113F45; EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                    100.0%; Score 124; DB 2;
11arity 100.0%; Pred. No. 6.8e-12;
Conservative 0; Mismatches 0:
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Best Local Similarity
Matches 25; Conserv
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hes 25; Conserv
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A,Status: preliminary
A,Molecule type: mRNA
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S26804
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Matches

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A;Cross-references: UNIPARC:UP1000011662A; EMBL:231383; NID:9472978; PIDN:CAA83258.1; PI C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-97/Domain: immunoglobulin homology <IMM>
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R; Paterson, G; Wilson, G; Kennedy, P.G.E.; Willison, H.J.
submitted to the RMBL Data Library, June 1995
A; Description: Analysis of anti-GMI ganglioside IgM antibodies cloned from motor neuropa A; Reference number: S57408
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A;Residues: 1-115 <PAT>
A;Cross-references: UNIPARC:UP100001137AD; EMBL:X87897; NID:9871273; PIDN:CAA61148.1; PI
                                                                                                                                                                                                                                                                                                                                                             C;Accession: S44125

R;Hawkins, R.B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idlotypic vaccination against human B-cell lymphoma: rescue of variable A;Reference number: S44105
A;Accession: S44125
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C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                               ominio chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
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Pred. No. 2.1e-11;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-99/Domain: immunoglobulin homology <1MM>
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96.0%; Pred. No. 2e-11;
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1 Similarity 96.0%;
24; Conservative 1
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Best Local Similarity 96.0%;
Matches 24; Conservative
                               24; Conservative
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Best Local Similarity
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Matches 24; Conserv
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A; Residues: 1-105 < HAW>
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Ig heavy chain V region (4.22) - human

C; Species Homo sapiens (man)

C; Species Homo sapiens (man)

C; Species Homo sapiens (man)

C; Saze Homo sapiens (man)

C; Saze Homo sizati

R; Sazz I : Kelly, P: Williams, C:; Scholl, S:; Tucker, P:; Capra, J.D.

R; Sazz, I: Kelly, P:; Williams, C:; Scholl, S:; Tucker, P:; Capra, J.D.

R; Sazz, I: Resident Homan V(H) gene families display remarkably little polymorphism.

A; Reference number: S09421; WUID:90059975; PMID:2511001

A; Reference number: S09421; MUID:90059975; PMID:2511001

A; Residues: preliminary; translation not shown

A; Residues: L'98 cSAN

A; Cross-references: UNIPARC:UPI0000176863; EMBL:X56365

C; Superfamally: immunoglobulin V region; immunoglobulin homology

C; Koywords: heteroctetramer; immunoglobulin homology < IMM>

F; 15-98/Domain: immunoglobulin homology < IMM>
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                                                                                                                                A; Accession: PH0876
A; Molecule type: DNA
A; Molecule the authors translated the codon TAT for residue 50 as Thr
C; Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C; Superfamily: immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology cIMM>
F; 15-97 Domain: immunoglobulin homology cIMM>
F; 15-37 Domain: immunoglobulin homology cIMM>
F; 15-37 Megion: complementarity-determining 2
F; 48-66/Region: complementarity-determining 2
   R; Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B. J. Exp. Med. 174, 1639-1652, 1991
A; Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype A; Reference number: PH0862; MUID:92078875; PMID:1660528
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Pred. No. 1.9e-11;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 99
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Pred. No. 1.9e-11;
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Local Similarity 96.0%;
nes 24; Conservative
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Local Similarity 96.0%;
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A;Residues: 1-99 <WEN>
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Best Loc Matches

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Gaps

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**Query Match** 

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1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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Job time : 21.2264 Becs
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518557
Ig heavy chain V region precursor (VIV-4) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: 318557
R;Shin, B.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, B.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physicial map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Title: Physicial map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Accession: 818557
A;Accession: 818557
A;Accession: 818557
A;Accession: 1-16 <&HI>
A;Residues: 1-116 <&HI>
A;Cross-references: UNIPARC:UPIO000115FF0; EMBL:X62112; NID:g37853; PIDN:CAA44022.1; PIL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin predicted <&IG>
F;20-116/Product: Ig heavy chain V region (VIV-4) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>
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S20780
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Decies: Homo sapiens (man)
C;Decies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20780
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Beference number: S20764
A;Reference number: S20764
A;Reference: UNIPARC:UP100001163F6; EMBL:Z1195B; NID:G33893; PIDN:CAA78015.1; PID:C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hererotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
A;Title: Organization and evolution of variable region genes of the human immunoglobulin A;Reference number: A26340; MUD:87051007; PMID:3097326
A,Accession: B26340
A,Accession: B26340
A,Accession: B26340
A,Residues: 1-116
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96.0%; Pred. No. 2.3e-11;
tive 1; Mismatches 0; Indels
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R;Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T. J. Mol. Biol. 190, 529-541, 1986
A;Title: Organization and evolution of variable region genes of the human immunoglobulin A;Reference number: A26340; MUID:87061007; PMID:3097326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Cross-references: UNIPARC: UPI000011641A, EMBL: Z12366; NID: 932950; PIDN: CAA78236.1; PID
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                                                                                                                                                                                                                                                                                                     N.Alternate names: Ig heavy chain V region (DP-66)
C.Species: Homo sapiens (man)
C.Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C.Accession: A26340; S26901
                                                       Gapa
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C;Keywords: heterotetramer; immunoglobulin
F;1.19/Domain: signal sequence #status predicted <SIG>
F;20-118/Product: Ig heavy chain V.II region 71-2 #status predicted <WAT>
F;30-118/Domain: immunoglobulin homology <IMN>
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     Length 118;
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  Score 121; DB 2;
Pred. No. 2.4e-11;
                                                                                                                                                                                                                                                                                   Ig heavy chain precursor V-II region (71-2) - human
                                                    1; Mismatches
                                                                                                         1 QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                                                                                                 QVQLQBSGPGLVKPSETLSLTCTVS 25
97.6%;
  Query Match
Best Local Similarity 96.09
Matches 24; Conservative
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A; Residues: 20-118 <TOM>
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 25, 2006, 06:05:44; Search time 133.491 Seconds (without alignments) 132.131 Million cell updates/sec Run on:

US-10-764-428-2 124 1 QVQLQESGPGLVKPSQTLSLTCTVS 25 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 Total number of hits satisfying chosen parameters:

2166443 seqs, 705528306 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ΩI	Q6GMX1_HUMAN	Q72379 HUMAN	Q9UL73 HUMAN	Q86SX2 HUMAN	QGGMX6_HUMAN	QGGMX7_HUMAN	Q96BY0 HUMAN	Q8IZD7_HUMAN	Q72374_HUMAN	Q510J1_RAT	HV2G_HUMAN	Q9UL75 HUMAN	095973_HUMAN	Q5M839_RAT	QSIOL9_RAT	Q6NYH3_HUMAN	O6P4I8 HUMAN	Q96KX8_HUMAN	Q569B8_RAT	Q569B6_RAT	Q53VQ0_MOUSB	Q53VQ4_MOUSE	Q53VQ8_MOUSE	Q53VR2_MOUSB	HV47 MOUSE	HV44_MOUSE	Q53VQ1_MOUSE	HV60_MOUSE	Q53VQ5_MOUSE	Q53VQ9_MOUSE	Q53VR3_MOUSE
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	Query Match	100.0	100.0	97.6	97.6	97.6	97.6	97.6	95.2	95.2	93.5	92.7	92.7	91.9	91.1	91.1	90.3	90.3	88.7	88.7	88.7	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1
	Score	124	124	121	121	121	121	121	118	118	116	115	115	114	113	113	112	112	110	110	110	108	108	108	108	108	108	108	108	108	108	108
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RESULT 2

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Homo sapiens (human) (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line) of
                                                                                                                                                                                                                                                                         Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=2511001;
Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.;
"The smaller human VH gene families display remarkably little
                                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                      Diamond B.;
"Molecular characteristics of antibodies bearing an anti-DNA-
associated idiotype.";
J. Exp. Med. 174:1639-1652(1991).
NUCLEOTIDE SEQUENCE.
MEDILINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; MAU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.6%; Score 121; DB 2; Length 119; 96.0%; Pred. No. 1.1e-10; Live 1; Mismatches 0; Indels
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Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                               Clin. Immunol. Immunopathol. 87:184-192(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBO J. 8:3741-3748(1989).
EMBL, AF035041; AAD56277.1; -; mRNA.
PIR; PHO876; PHO876.
PIR; S12416; S12416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P01820; 1G7J.
SMR; Q9UL73; 1-119.
InterPro: IPR007110; Ig-like.
InterPro: IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4

Q865XZ HUMAN
DG65XZ HUMAN PRELIMINARY;
AC Q865XZ;
DT 01-JUN-2003 (TrEMBLrel. 24,
DT 01-JUN-2003 (TrEMBLrel. 24,
DT 01-JUN-2003 (TrEMBLrel. 24,
DT 01-JUN-2003 (TrEMBLrel. 26,
DE Pull-length CDNA clone CSODI
DE Homo sapiens (human) (Fragme
OS Homo sapiens (human) (Fragme
OC Homo.

CC HOmo.

NCBI_TAXID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA LIM WB., GTUBER C., Jessee J
RL SUDMITTER (FRB-2003) to the
RN (12)
RN UCLEOTIDE SEQUENCE.
RC TISSUE= Cells;
RN (12)
RN (13)
RN (14)
RN (15)
RN (15)
RN (15)
RN (16)
RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Conservative
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                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymorphism."
                                                                                                                                                                                                                                                  PubMed=1660528
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SEQUENCE
                                                                                                                                           fetus.";
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Matches
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUR=Human rectum tumor;
A Bloecker H., Beecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Becher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BK338066; CAD97996.1; -; mRNA.
EMBL; BK338066; CAD97996.1; -; mRNA.
EMBL; BK380060; IG7J.

R Riscripto; IRNO0110076; Homo sapiens.

R InterPro; IPR003507; Ig-1.

R InterPro; IPR003507; Ig-1.

R InterPro; IPR003506; Ig-W.

R FinterPro; IPR003506; Ig-W.

R FinterPro; IRNO03507; Ig-V.

R FinterPro; IRNO03507; Ig-V.

R FinterPro; IRNO03507; Ig-V.
                                                                                                                                                                        Gaps
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                                                                                                                  Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                               Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478 AA; 51620 MW; 4APCB541F3217CA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothettal protein DKFZp686K04218 (Fragment).
                                                                                                         100.0%; Score 124; DB 2;
llarity 100.0%; Pred. No. 1.6e-10;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     478 AA.
                                                                                                                                                                                                                                                        20 QVQLQRSGPGLVKPSQTLSLTCTVS 44
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                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
     PROSITE, PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UL73_HUMAN PRELIMINARY;
Q9UL73;
                                                                                                                                                                                                                                                                                                                                                                                                               072379 HUMAN PRELIMINARY,
072379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
NON TER 1
SEQUENCE 478 AA;
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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NCBI_TaxID=9606;
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RESULT 3
409UL73 HU
AC Q9UL73 HU
AC Q9UL70 DT 01-N
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                                                                                                                 RESULT 6
QGGMX7 HU
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X TISSUB-Primary B-Cells;

X Statusberg R.L., Pelngold B.A., Grouse L.H., Derge J.G.,

RIJUNE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X RIJUNE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X RIJUNE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X RIJUNE R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Hischul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Toshiyuki S., Casavant T.L., Scheetz T.B.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Willalon D.K., Muzny D.W., Sodergen B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Mitting M., Madan A., Young A.C., Shevchenko Y., Boufer G.C.,

Blakesley R.W., Touchman J.W., Green B.D., Dickon M.C.,

Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Rochectt A., Schein J.B., Jones S.J.M., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                          Score 121; DB 2; Length 139;
Pred. No. 1.2e-10;
1; Mismatches 0; Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                     139 AA; 15573 MW; 7D1B2302410B4F8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                             465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC073766; AAH73766.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                 33 QVQLQESGPGLVKPSETLSLTCTVS 57
                                                                                                                                   1 QVQLQBSGPGLVKPSQTLSLTCTVS 25
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B
                                                                                                                                                                                                                                                      Created)
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InterPro; IPR007110; IG-11ke.
InterPro; IPR003597; IG.C1.
InterPro; IPR003006; IG.WHC.
InterPro; IPR003596; IG.W.
Pfam; PP07654; C1-8et; 3.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                           96.0%;
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                                                                                97.6%;
                                                                   Query Match
Best Local Similarity 96.04
                                                                                                                                                                                                                      QGGMX6_HUMAN PRELIMINARY;
QGGMX6;
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                              Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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RECEIVED SEQUENCE.

RECTISEDEPTIANS PLOBERS:

RECTISESPERIARY B-Cells;

RECTISESPERIARY B-Cells;

RECTISESPERIARY B-Cells;

RECTISESPERIARY B-Cells;

RECTISESPERIARY B-Cells;

RASEDING-SECOND BLOWN G. M., Derge J.G.,

RASEDING R.D., Collins F.S., Regner L., Shenmen C.M., Schuler G.D.,

RASEDING R.D., Collins F.S., Regner L., Scheefer C.F., Bhat N.K.,

RASEDING R.D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

By Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Perers G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robert S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robert S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia R.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia R.W., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhatesley R.W., Touchman J.W., Gren B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Gren B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Rodriguez A.C., Grimwood J., Schmutz J., Myerra R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Salacke L., Salacke L.,

Rodriguez A.C., Grimwood J., Salacke L., Salacke L.,

Rodriguez A.C., Grimwood J., Salacke L., Salacke L.,

Rodriguez
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Strausberg R:
Strausberg R:
Strausberg R:
Strausberg R:
Strausberg R:
Submitted (UW-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073765; AAH73765.1; -; mRNA.
SMR; OGGNX7; 247-455.
RIGHT COMMOTION:
RIGHT PRO01502; Cintegral to membrane; IEA.
RIGHT PRO01502; IG-11
RIGHT PRO01503; IG-11
RIGHT PRO01503; IG-11
RIGHT PRO01504; IG-14
RIGHT PRO0405; IG-14
REPRO0406; IG-14
REPRO0406; IG-14
REPRO0406; IG-14
REPROSTER; SMO0406; IG-13.
REPROSTER; PSC0290; IG-13.
REPROSTER; PSC0290; IG-14
REPROSTER; PSC0290; IG-14
REPROSTER; PSC0290; IG-16
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Query Match
97.6%; Score 121; DB 2; Length 465;
Best Local Similarity 96.0%; Pred. No. 4.6e-10;
Matches 24; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al protein. - 477 AA; 51631 MW; 9PB59C09C50CPP85 CRC64;
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05-ULL-2004 (TrEMBLrel. 27, Last sequence update)
05-ULL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo eaplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 AA
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                                                                                                                                                                                                                                                               1 OVOLORSGPGLVKPSQTLSLTCTVS 25
                                                                                                                                                                                                                                                                                                                                                     20 QVQLQESGPGLVKPSBTLSLTCTVS 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 HUMAN
QGGMX7 HUMAN PRELIMINARY;
QGGMX7;
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NCBI_TaxID=9606;
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MEDLINE-2188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-2288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Ridusper R.D., Colling F.S., Wargner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheefer T.E.,
Romstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,
Anting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,
Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Genertain and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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InterPro; IRR003599; IG.
InterPro; IRR003599; IG.
InterPro; IRR003599; IG.
InterPro; IRR003006; IG.
InterPro; IRR003596; IG.
InterPro; IRR003596; IG.
InterPro; IRR003596; IG.
InterPro; IRR00409; IG.
SMART; SM00409; IG.
SMART; SM00406; IGV; I.
PROSITE; PSO0359; IG HIC; UNKNOWN 3.
SEQUENCE 620 AA; 68125 MW; 990A1A4A6EBFF27B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                          620 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            extremely heterogeneous at the 5' end.";
Nucleic Acids Res. 19:2427-2433(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC011857; AAH11857.2; -; mRNA.
PIR; S15590; S15590.
HSSP; OD1820; 1G7J.
SMR; Q96EY0; 27-251.
Ensembl; ENSG0000130076; Homo sapiens.
QVQLQESGPGLVKPSETLSLTCTVS 44
                                                                                                            PRT;
                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                        Q96EYO HUMAN PRELIMINARY;
Q96EYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Primary B-Cells;
NIH MGC Project;
                                                                                                                                                                                                                                     Homo sapiens (Human)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686C0218 (Fragment).
Name=DKFZp686C02218;
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                    Gaps
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Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Boecher M., Memann S.;
Submitted (Jun-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BX538077; CAD98001.1; -; mRNA.
HSSP; P01820; 1G7J.
BNSF, P01820; 1G7J.
Bnsembl; ENSG0000013076; Homo sapiens.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig_c1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 130;
Score 121; DB 2; Length 620;
Pred. No. 6.3e-10;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-thyroglobulin heavy chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                Jang Y.-J., Chung J., Park J.-Y.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY145445; AAN64329.1; -; mRNA.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 AA; 13901 MW; 036131FC6EC1551E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 95.2%; Score 118; DB 2; Local Similarity 92.0%; Pred. No. 3.4e-10; Nes 23; Conservative 2; Mismatches 0;
                                                                                                                                                                                     130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMR; Q81ZD7; 1-130.
Ensembl; ENSG00000130076; Homo sapiens
                                                                   1 QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                                                    1 QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQQSGPGLVKPSETLSLTCTVS 25
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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PROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
Query Match 97.6%;
Best Local Similarity 96.0%;
Matches 24; Conservative 1
                                                                                                                                                                  Q7Z374_HUMAN PRELIMINARY;
Q7Z374;
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                                                                                                                                                     RESULT 8
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HV2G_HUMAN
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MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Itachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hoog L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hoog L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hoog L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Carahni P. Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha S.B., McKerman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

B Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                              Gaps
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NIH MGC Project;

Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.

REMBL; BC008269; AR488269.1; -; MRNA.

GO; GO:0003823; F:antigen binding; IEA.

R InterPro; IPR003599; Ig.

R InterPro; IPR003100; Ig-1ike.

R InterPro; IPR003597; Ig-c1.

R InterPro; IPR003597; Ig-c1.

R InterPro; IPR003597; Ig-c1.

R InterPro; IPR003596; Ig-c1.

R InterPro; IPR003596; Ig-c1.

R SWART; SM00409; IG; 3.

SWART; SM00407; IGc1; 3.
                                                                                                                                                                                                            Score 118; DB 2; Length 492;
Pred. No. 1.4e-09;
2; Mismatches 0; Indels
                                                                                                                                                                   492 AA; 53776 MW; 1B7A15760F0CA74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 AA
                                                                                                                                                                                                                                                                                                       Created)
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PR07654; C1-8et; Z.
SMART; SM00406; IGv; IIKR; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                   y Match
Local Similarity 92.0%;
les 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSIOJI_RAT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                   Hypothetical protein.
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                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                         Query Match
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OSIOJI RAT
10-MA
DT 00510J
AC 0510J
AC 0510J
DD 110-MA
DT 110-MA
DA NALSC
RA HODKI
RA BLAKE
RA BLA
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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R PDB; TRAB; X-ray; H=2-117.

R PDB; TRAB; X-ray; H=2-117.

DR GO; GO:0005576; C:extracellular region; NAS.

DR GO; GO:000555; P:immure response; NAS.

DR GO; GO:0006595; P:immure response; NAS.

DR InterPro; IPR003196; Ig-like.

DR InterPro; IPR003196; Ig-like.

DR RNRT; SM00406; IGV; 1.

DR RNSTIR; PSS5085; IG-LIKE; 1.

DR PR0STIR; PSS5085; IG-LIKE; 1.

DR PR0STIR; PSS5085; IG-LIKE; 1.

DR RNSTIR; PSS085; IG-LIKE; 1.

Pyrrolidone carboxylic acid.
                                                                                                                                                                                        Gaps
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Saul F.A., Amzel L.M., Poljak R.J.;
Saul F.A., Amzel L.M., Poljak R.J.;
"Prealiminary refinement and structural analysis of the Pab fragment from human immunoglobulin new at 2.0-A resolution.";
J. Biol. Chem. 253:585-597(1978).
-i. MISCELLANBOUS: This chain was isolated from an IgG1 myeloma
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-!- SIMILARITY: Contains 1 1g-like (immunoglobulin-like) domain.
                                                                                                                                                                                        ö
                                                                                                                          Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=77242302; PubMed=407927; Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.; Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.; Anino acid sequence of the VH region of a human myeloma immunoglobulin (IgG New) "; Biochemistry 16:3412-3420(1977).
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 477 AA; 52167 MW; 226460762898C6F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT
                                                                                                                       Score 116; DB 2; Lv
Pred. No. 2.9e-09;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-071-1986 (Rel. 01, Created)
21-071-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
II heavy chain V-II region NEWM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA.
                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                                                                                                                                                                                                                                                      20 QVQLKESGPGLVQPSQTLSLFCTVS 44
                                                                                                                                 93.5%;
                                                                                                                              Query Match
Best Local Similarity 92.0°
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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P01825;
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MEDLINE=93101610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
MEDLINE=93101610; Marx N.S., Oppliger I.R., Mannik M., Sasso E.H.;
Hillson J.L., Karr N.S., Oppliger I.R., Mannik M., Sasso E.H.;
Hillson J.L., Karr N.S., Oppliger I.R., Mannic M., Sasso E.H.;
The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A.";
J. Exp. Med. 178:331-336(1993).

R EMBL, AR035039; AAD56275.1; -; mRNA.
R PIR; PH1674; PH1674.
R PIR; PL0117; PL0117.
R PIR; PL01160; PL01160.
R PIR; PS0089; PS0089.
R PIR; PS0090; PS0090.
R PIR; S12433; 512433.
R PIR; S12433; 512433.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
"Clonal proliferation of IgM secreting B cell in the synovium of
Behcet's patient with arthritis.";
                                                                                                                                                                                                                                                                                                                                                                Length 122;
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                                                                                                                                                                                                                                                                                                                                    122 AA; 13719 MW; 56CB0612586A6529 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) WH4 heavy chain variable region precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                              / Match 92.7%; Score 115; DB 2; L. Local Similarity 88.0%; Pred. No. 9.4e-10; nes 22; Conservative 2; Mismatches 1;
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01-MAY-1999 (TrEMBLrel. 10, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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HSSP, P01220; 1G7J.
SWR, 095973; 20-147.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PR053TB; PS50835; IG_LIKB; 1.
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PROSITE; PS50835; IG_LIKE; 1.
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PIR; S78056; S78056.
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NCBI_TaxID=9606;
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Logtenberg T., Young F.M., Van Es J.H., Gmelig-Meyling F.H., Alt F.W.;
"Autoantibodies encoded by the most Jh-proximal human immunoglobulin
heavy chain variable region gene.";
J. Exp. Med. 170:1347-1355(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Schroeder H.W. Jr, Wang J.Y.;
"Preferential utilization of conserved immunoglobulin heavy chain
variable gene segmente during human fetal life.";
Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).
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Bird J., Galili N., Link M., Stites D., Sklar J.;
Continuing rearrangement but absence of somatic hypermutation in immunoglobulin genes of human B cell precursor leukemia.";
J. Exp. Med. 168:229-245(1988).
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                                                                                                                                                                                                                     ö
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                                                                                                                                                                                        DB 1; Length 117;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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                                                                                                                                                             12790 MW; 2DA47B509562D237 CRC64;
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Pred. No. 9e-10;
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88.0%;
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Best Local Similarity 80...
Best Local 22, Conservative
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Q9UL75;
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SEQUENCE
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Best Local Similarity 88.03
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
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           Potential.
VH4 heavy chain variable region.
                                                                                                                                           Length 150;
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Director MGC Project;
Bubmitred (DRC-2004) to the EMBL/GenBank/DDBJ databases.
Submitred (DRC-3004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC088254; AAH88254.1; -; mRNA.
GO; GO:0003823; F:antigen binding; IEA.
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51403 MW; 030A2C3C66228F16 CRC64;
             1 19 Potential.
20 >150 VH4 heavy chain variable 3
150 Ap. 16315 MW, 85664E04938AA7C9 CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                      Score 114; DB 2;
Pred. No. 1.7e-09;
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                                                                                                                                                                                                 3; Mismatches
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InterPro; IPR007110; IG-11ke.
InterPro; IPR003597; IG.1.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_W.
Pfam; PP07654; C1-8et; 3.
                                                                                                                                      91.9%;
88.0%;
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PROSITE; PS00290; IG_MHC; UNK
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01-FEB-2005 (TrEMBLrel. 29,
01-FEB-2005 (TrEMBLrel. 29,
19h-1a predicted protein.
Name-19h-1a predicted;
                                                                                                                        Query Match
Best Local Similarity 88.0*
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QSM839;
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SMART; SM00407; IGC1; 3
SMART; SM00406; IGV; 1.
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Length 469;

DB 2;

91.1%; Score 113;

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XX Straublers R.L., Feingold B.A., Groube L.H., Derge J.G.,

XR Straubberg R.L., Feingold B.A., Groube L.H., Derge J.G.,

X Strauberg R.L., Feingold B.A., Groube L.H., Derge J.G.,

X Lausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Distchenko L., Maruelina K., Farmer A.A., Rubin G.M., Hong L.,

X Distchenko L., Maruelina R., Farmer A.A., Rubin G.M., Hong L.,

X Distchenko L., Maruelina R., Farmer A.A., Rubin G.M., Hong L.,

X Stapleton M.J., Uddin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.W.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X Villalon D.K., Muzny D.W., Green R.D., Dickson M.C.,

X Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Rodriguez A.C., Girlmwood J.W., Green R.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E.,

X TGeneration and initial analysis of more than 15,000 full-length human
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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NIH MGC Project;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC088184; AAH88184.1; -; mRNA.
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Last annotation update)
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88.0%; Pred. No. 1.1e-08;
iive 3; Mismatches 0;
88.0%; Pred. No. 8.3e-09; ive 3; Mismatches 0
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SMART; SM00407; IGC1; 4.
SMART; SM00408; IGC2; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIXE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
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10-MAY-2005 (TrEMBLrel. 30, Le
10-MAY-2005 (TrEMBLrel. 30, Le
LOC366747 protein (Fragment).
Name=LOC366747;
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InterPro; IPR007110; Ig-like.
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Interpro; IPR003598; Ig_C2.
Interpro; IPR003506; Ig_MHC.
Interpro; IPR003596; Ig_V.
Pfam; PP07654; C1-8et; 4.
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Matches 22; Conservative
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QSIOL9 RAT
ID QSIOL9 RAT PRELIMINARY;
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NCBI_TaxID=10116;
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                                                           April 25, 2006, 06:58:17; Search time 108.962 Seconds (without alignments) 95.866 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*):

(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*):

(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*):
           GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-783-950-137
US-10-994-9608-249
US-10-984-9608-57
US-10-171-681-19
US-10-171-680-19
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US-10-194-975-36
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US-10-194-975-39
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US-10-453-698-81
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US-10-029-926B-90
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                                                                                                                                                          1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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28 124 100.0 99 4 US-10-379-392-45 Sequence 45, Appl 29 124 100.0 99 4 US-10-379-392-46 Sequence 46, Appl 30 124 100.0 99 5 US-10-944-965 Sequence 46, Appl 30 124 100.0 107 3 US-10-944-96678-82 Sequence 47.4 Appl 32 124 100.0 110 4 US-10-309-762-74 Sequence 74, Appl 34 124 100.0 110 5 US-10-309-762-74 Sequence 77, Appl 35 124 100.0 117 4 US-10-310-613-5 Sequence 5, Appl 36 124 100.0 117 4 US-10-310-613-5 Sequence 13, Appl 39 124 100.0 117 4 US-10-310-53-5 Sequence 13, Appl 40 124 100.0 117 4 US-10-310-53-5 Sequence 13, Appl 41 124 100.0 117 5 US-10-60-357-5 Sequence 13, Appl 41 124 100.0 117 5 US-10-738-916A-72 Sequence 5, Appl 41 124 100.0 118 4 US-10-078-757B-50 Sequence 5, Appl 41 124 100.0 118 4 US-10-078-757B-50 Sequence 13, Appl 42 100.0 118 4 US-10-078-757B-50 Sequence 13, Appl 42 100.0 118 4 US-10-078-757B-50 Sequence 13, Appl 42 100.0 119 4 US-10-330-613-25 Sequence 25, Appl 42 124 100.0 119 4 US-10-330-613-25 Sequence 25, Appl 44 124 100.0 119 4 US-10-330-613-25 Sequence 25, Appl 45 124 100.0 119 4 US-10-330-613-25
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  25; Conservative
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CORGANISM: Homo sapiens
US-10-783-950-137
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; ORGANISM: Homo sapien
US-09-563-222-146
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US-10-923-068-249
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Sequence 28, Application Wo. US20030012781A1

Sequence 28, Application No. US20030012781A1

GENERAL INFORMATION:

APPLICANT: ANDERSON, DARRELL

APPLICANT: HANNA, NABIL

APPLICANT: CONTAINING, AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF

FILE REFERENCE: 037003-0280632

CURRENT APPLICATION NUMBER: US/09/874,141

CURRENT PILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 28

LENGTH: 30
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Sequence 29, Application No. US20030012781A1

SEQUENCE 29, Application No. US20030012781A1

GENERAL INFORMATION:

APPLICANT: HANNA, NABIL

APPLICANT: HANNA, NABIL

APPLICANT: HASTETTER, WILLIAM H.

APPLICANT: KLOSTZER, WILLIAM S.

TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS

TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: 1037003-0280632

CURRENT APPLICATION NUMBER: US/09/874,141

PRIOR PELICATION NUMBER: 60/209,584

PRIOR FILING DATE: 2000-06-06

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PATENTIN VET. 2.1

SEQ ID NO 29

LENGTH: 30
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                                                               Query Match
100.0%; Score 124; DB 5;
Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 25; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 25; Conservative
    ; ORGANISM: Homo sapiens
US-10-923-068-381
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-874-141-29
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Best Local Similarity
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US-09-874-141-29
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Sequence 137, Application US/10783950

Sequence 137, Application No. US2004019945A1

GENERAL INFORMATION:
APPLICANT: BEICTTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
TITLE OF INVENTION: INMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
TITLE REPERENCE: 068904-0501
CURRENT APPLICATION NUMBER: US/10/783,950
CURRENT FILING DATE: 2000-05-19
FRIOR PILING DATE: 2000-05-02
FRIOR PILING DATE: 2000-05-02
FRIOR PILING DATE: 2000-05-02
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Publication No. US20030079253A1

GENERAL INFORMATION:

APPLICANT: Hatt, Andrew

APPLICANT: Hein, Mich B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN

TITLE OF INVENTION: BUCKARYOTIC CELLS

FILE REFERENCE: 310098 406

CURRENT APPLICANTON UNDERS: US/09/563,222

CURRENT PLLING DATE: 2000-05-02

NUMBER OF SEQ ID NOS: 197

SEQ ID NO 146

LENGTH: 30
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2004-11-08

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CURRENT FILING DATE:
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US-10-171-681-19
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US-10-984-960A-21

Sequence 21, Application US/10984960A

Publication No. US20050142137A1

Publication No. US20050142137A1

GENERAL INFORMATION:

APPLICANT: Chui, Daniel

APPLICANT: Choi, Haihong

APPLICANT: LaRcohalle, William J.

APPLICANT: Ara, Gulshan

CURRENT: PLINE OF INVENTION: AND ARE: US, 10/984, 960A

CURRENT APPLICATION NUMBER: US, 10/984, 960A

CURRENT PILING DATE: 2003-11-07

NUMBER OF SEQ ID NOS: 112

SOFTWARE: CuraSeqList version 0.1

SEQ ID NO 21

LEGGTH: 30

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LEGGTH: APPLICATION OF SEQ ID NOS: 112

SEQ ID NO 21

LEGGTH: 30
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Publication No. US20050142137A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallo, Michael
APPLICANT: Shong, Hailhong
APPLICANT: Ara, Gulshan
APPLICANT: LaRochelle, William J.
APPLICANT: LaRochelle, William J.
APPLICANT: LAROCHELLE ANTHEODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
FILE REPERENCE: Cura 970
CURRENT APPLICATION NUMBER: US/10/984,960A
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Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0;
Sequence 249, Application US/10923068
Publication No. US20050042664A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Damschroder, William
APPLICANT: Damschroder, Melissa
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOPTWARE: FastSEQ for Windows Version 4.0
IENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-10-923-068-249
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US-10-984-960A-57
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US-10-171-681-19
US-10-171-681-19
US-10-171-681-19
Sequence 13, Application US/10171681
Sequence 13, No. U3203017023341
Sequence 13, No. U3203017023341
Septicant No. U3203017023341
APPLICANT BLACK, Amelia
APPLICANT HANNA, Nabil
APPLICANT NEWAN, Nabil
APPLICANT COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN 9D39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN 9D39,
TITLE OF INVENTION: Doane, Swecker & Mathis
STREET: P.O. Box 1404
STREET: P
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100.0%; Score 124; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 1.16-10;
Matches 25; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/518,275
PRIOR PLING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 112
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 57
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-10-984-960A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQRSGPGLVKPSQTLSLTCTVS 25
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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WESULO 13

WESULO 13

Sequence 20, Application US/10171680

Sequence 20, Application US/10171680

PUBLICANT: BLACK, Amelia

APPLICANT: BLACK, Amelia

APPLICANT: HANNA, Mabil

APPLICANT: HANNA, Mabil

APPLICANT: WEWMAN, Roland A.

TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 28

CORRESPONDENCES: 28

CORRESPONDENCES: 28

CORRESPONDENCES: 28

CORRESPONDENCES: 28

CONTRY: United States

STATE: Virginia

STATE: Virginia

STATE: Virginia

STATE: Virginia

COUNTRY: United States

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: BEN PC COMPATION: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 87;
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   TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THER NUMBER OF SEQUENCES: 28
CORRESPONDENCES: 28
CORRESPONDENCES:
ADDRESSER: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STREET: Virginia COUNTRY: United States
ZIP: 22313-1404
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/NS-DOS SOFTWARE: Patentl Nelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/171,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 124; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: TESKIM, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELEFORMUNICATION INFORMATION:
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
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APPLICATION NUMBER: US/08/554,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRICA APPLICATION DATA:
APPLICATION NUMBER: 09/332,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
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APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: HANNA, Nabil
APPLICANT: HANNA, Nabil
APPLICANT: HANNA, Nabil
APPLICANT: NEWMAN, Reland A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
ITILE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STREET: P.O. Box 1404
COUNTRY: United States
ZIP: Z2313-1404
COUNTRY: United States
ZIP: Z2313-1404
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE PC-DOSA MS-DOS
CONTANDED: DETAILS 
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APPLICANT: PADLAN, Eduardo A.
APPLICANT: PERMAN, ROLand A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTAR: ALC. ALC. ALC. ALC. ALC. COMPUTAR: ALC. DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/171,681 FILING DATE: 17-JUNE-2001 CLASSIFICATION DATA: APPLICATION NUMBER: US/08/925,339 FILING DATE: WORDER: US/08/925,339 FILING DATE: US/08/925,339 FILING DATE: US/08/925 WARE: TELENGATION NUMBER: US/08/954,840 FILING DATE: US-NOV-1995 ATTORNEY/AGENT INFORMATION: NAME: Teskin, Robin L. REGISTRATION NUMBER: 012712-127 FELECOMMINICATION INFORMATION: TELECOMMINICATION INFORMATION: TELECOMMINICATION INFORMATION: TELECOMMINICATION INFORMATION: TELECOMMINICATION INFORMATION: TELECOMMINICATION INFORMATION: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 87 aming acide
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                       QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                                                    QVQLQESGPGLVKPSQTLSLTCTVS 25
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Sequence 19, Application US/10171680
Publication No. US20030175269A1
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
                                                                                                                                                                                                                                                                        Sequence 20, Application US/10171681 Publication No. US20030170233A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 25; Conservative
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STRANDEDNESS: single
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Gaps

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Search completed: April 25, 2006, 07:08:49 Job time : 109.962 Becs
                                                                                    TYPE: PRT ORGANISM: Homo sapiens US-10-194-975-38
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Best Local Similarity 100.0%; Pred. No. 4.1e-10;
Matches 25; Conservative 0; Mismatches 0;
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US-10-194-975-38
US-10-194-975-38

§ Sequence 38, Application US/10194975

§ Publication No. US20030039649A1

§ GENERAL INFORMATION:

§ APPLICANT: Foote, Jefferson

§ TITLE OF INVENTION: Super Humanized Antibodies

§ CURRENT APPLICATION NUMBER: US/10/194,975

§ CURRENT FILING DATE: 2002-10-10

§ PRIOR APPLICATION NUMBER: US 60/305,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-10-194-975-36

Sequence 36, Application US/10194975

Publication No. US20030039649A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01

CURRENT PRILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US/10/194,975

CURRENT PRILING DATE: 2001-07

PRIOR PILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 122

SEQ ID NO 36

LENGTH: 99
                  FILING DATE:
CLASSIFCATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/332,595
FILING DATE:
APPLICATION NUMBER: 08/08/554,840
FILING DATE:
ATOCNEY AGENT INPORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION SA5-620
INPORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 anino acids
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APPLICATION NUMBER: US/10/171,680
                                                                                                                                                                                                                                                                                                                                                                 TYPE: maino acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 25, Conserva
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PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 38
LENGTH: 99
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US-11-054-669-36
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1. /SIDS5/ptodata/1/pubpaa/USO8 NEW FUB.pep:*
2. /SIDS5/ptodata/1/pubpaa/USO7.NEW FUB.pep:*
3. /SIDS5/ptodata/1/pubpaa/PCT_NEW FUB.pep:*
4. /SIDS5/ptodata/1/pubpaa/PCT_NEW FUB.pep:*
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6. /SIDS5/ptodata/1/pubpaa/USO1 NEW FUB.pep:*
7. /SIDS5/ptodata/1/pubpaa/USO1 NEW FUB.pep:*
8. /SIDS5/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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124
1 QVQLQBSGPGLVKPSQTLSLTCTVS 25
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIE

SUMMARIES	Description	US-11-054-669-36 Sequence 36, App.	m	39,	20,	42,	Sequence 43,	0 Sequence 50	1-012-353-72 Sequence 72, Appl	10-530-171-7 Sequence 7, Ap	11-004-590-237 Sequence 237, App	US-11-004-590-331 Sequence 331,	Sequence	11-004-590-342 Sequence 342,	11-004-590-348 Seguence 348,	Sequence	Sequence	11-004-590-369 Sequence 369,	7	US-11-266-444-1960 Sequence 1960,	1-054-515-1962 Sequence 1962,	196	Sequence 161	1619	1-144-248-36 Sequence 36, Appl	
os	a	US-11	US-11	US-11	US-11	US-11	US-11		US-11	US-10	US-11	US-11	US-11	US-11	US-11	US-11	_	US-11	US-11	US-11	US-11	US-11	US-11	US-11	US-11	
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	* Query Match Length DB	99	66	66	66	66	66	66	117	119	119	119	119	119	119	119	119	119	248	248	249	249	253	253	97	
٠	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	97.6	
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Sequence 42, Appl Sequence 51, Appl Sequence 51, Appl Sequence 54, Appl Sequence 54, Appl Sequence 46, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 74, Appl Sequence 67, Appl Sequence 55, Appl Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli
US-11-054-669-42 US-11-054-669-51 US-11-084-554-53 US-11-084-554-54 US-11-084-554-54 US-11-084-522-46 US-11-144-222-46 US-11-136-222-46 US-11-136-223-46 US-11-182-343-36 US-11-182-343-44 US-11-054-669-43 US-11-054-669-43 US-11-054-669-43 US-11-054-669-43 US-11-054-669-43 US-11-094-599-866-6 US-11-0938-005B-36
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US-11.084-554-50

Sequence 50, Application US/11084554

Publication No. US20050260679A1

SEGNERAL INFORMATION:

APPLICANT: Kellermann, Sirid-Ai

APPLICANT: Green, Larry L.

APPLICANT: Kellermann, Sirid-Ai

APPLICANT: MANTHODIES THROUGH V GENE MANIPULATION

FILE REFERENCE: ABGENIX.100A

CURRENT FILING DATE: 2005-03-17

PRIOR APPLICATION NUMBER: 60/554,372

PRIOR APPLICATION NUMBER: 60/554,372

PRIOR APPLICATION NUMBER: 60/554,61

PRIOR APPLICATION NUMBER: 60/554,61

PRIOR APPLICATION NUMBER: 60/574,661

PRIOR PLING DATE: 2004-05-24

NUMBER OF SEQ ID NOS: 266

SEQ ID NO 50

LENGTH: 99
                                                                                                                                 Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 124; DB 7; Length 99; Best Local Similarity 100.0%; Pred. No. 2.6e-11; Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                              Query Match
100.0%; Score 124; DB 7;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 0; Mismatches 0;
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Sequence 39, Application US/11054669

Sequence 39, Application US/11054669

Publication No. US2050261480A1

GENERAL INFORMATION:

APPLICANT: FOOLE, Jefferson

TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES

FILE REFERENCE: 3019/US/3

CURRENT APPLICATION NUMBER: US/11/054,669

CURRENT PILING DATE: 2005-02-08

PRIOR PILING DATE: 2002-07-12

PRIOR PILING DATE: 2001-07-12

PRIOR PILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 124

SEQ ID NO 39

LENGTH: 99
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Best Local Similarity 100.0
Matches 25; Conservative
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-38
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US-11-054-669-39
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ORGANISM: Homo sapiens
US-11-084-554-50
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US-11-004-590-43

US-11-004-590-43

Sequence 43, Application US/11004590

Publication No. USZ006000883A1

GENERAL INFORMATION:

APPLICANT: Lazar, Greecy Alan

APPLICANT: Desjarlais, John R.

APPLICANT: Hammond, Phillip W.

ITILE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF

ITILE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF

FILE REFERENCE: 185832/US/5

CURRENT APPLICATION NUMBER: US/11/004,590

CURRENT FILING DATE: 2004-12-03

PRIOR FILING DATE: 2004-12-04

PRIOR FILING DATE: 2004-06-21

PRIOR PILING DATE: 2004-08-13

PRIOR PILING DATE: 2004-08-13
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QVQLQESGPGLVKPSQTLSLTCTVS 25
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US-11-004-590-42
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US-11-004-590-43
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TYPE: PRT
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                                                     Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kellermann, Sirid-Ai
APPLICANT: Kellermann, Sirid-Ai
APPLICANT: Korver, Wouter
ITILE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
FILE REFERENCE: ABGENIX.100A2
CURRENT APPLICATION NUMBER: US/11/136,250
CURRENT PILING DATE: 2005-05-23
FRIOR APPLICATION NUMBER: 11/084,554
FRIOR APPLICATION NUMBER: EVT/US2005/009306
FRIOR FILING DATE: 2005-03-17
FRIOR FILING DATE: 2004-03-17
FRIOR APPLICATION NUMBER: 60/574,661
FRIOR FILING DATE: 2004-03-19
FRIOR FILING DATE: 2004-03-19
FRIOR APPLICATION NUMBER: 60/554,372
FRIOR FILING DATE: 2004-03-19
FRIOR FILING DATE: 2004-03-19
SUMBER OF SEQ ID NOS: 266
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 50
LENGTH: 99
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Query Match 100.0%; Score 124; DB 7; Length 99; Best Local Similarity 100.0%; Pred. No. 2.6e-11; Matches 25; Conservative 0; Mismatches 0; Indels
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CURRENT PILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/75,916
PRIOR PILING DATE: 2003-12-16
PRIOR PLICATION NUMBER: PR 0308538
PRIOR PILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PT/PR03/00178
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-05-07
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORVAIÀ, NATHALIB
DUFLOS, ALAIN
HAEUW, JEAN-FRANCOIS
IEGER, OLIVIER
BECK, ALAIN
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    TYPE: PRT
    ORGANISM: Homo sapiens
US-11-136-250-50

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Best Local Similarity
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APPLICANT:
APPLICANT:
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Sequence 237, Application US/11004590
Publication No. US2006000883A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John R.
APPLICANT: Hammond, Phillip W.
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
CURRENT APPLICATION NUMBER: US/11/004,590
CURRENT PILING DATE: 2004-12-03
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100.0%; Score 124; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels (
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APPLICANT: OIKE, Shinsuke
APPLICANT: OIKE, Shinsuke
APPLICANT: TAGAWA, TOSHIAKI
APPLICANT: HOSOKAWA, Saiko
APPLICANT: HOSOKAWA, Saiko
APPLICANT: HOSOKAWA, Saiko
TITLE OP INVENTION: Antibody recognizing antigen
FILE REFERENCE: 235054
FILE REFERENCE: 235054
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: US/10/530,171
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: US/2002/012732
PRIOR PILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
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                                                                                                                                                                                                                      ; LOCATION: (59)
; OTHER INFORMATION: Variable amino acid
US-11-012-353-72
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PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 72
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/10530171
Publication No. US20060057147A1
GENERAL INFORMATION:
APPLICANT: HIRAKAWA, Youko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Conservative
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US-10-530-171-7
                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 25; Conserv
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US-11-004-590-237
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APPLICANT: Lazar, Gregory Alan
APPLICANT: Lazar, Gregory Alan
APPLICANT: Lazar, Gregory Alan
APPLICANT: Lazar, Gregory Alan
APPLICANT: Lazar, Gregory Philib, Brille
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION WHORER: US 60/527,167
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR APPLICATION NUMBER: US 60/519,483
PRIOR PILING DATE: 2004-06-13
PRIOR PILING DATE: 2004-10-14
NUMBER OF SEQ ID NOS: 458
SOFTWARE PLENTED NOS: 458
SOFTWARE PREFERENT VERSION 3.3
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100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
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CONTENT AND COMPOSITIONS THEREOF
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             TITLE REFERENCE: 185922/US/5
CURRENT APPLICATION NUMBER: US/11/004,590
CURRENT FILING DATE: 2004-12-03
PRIOR PELICATION NUMBER: US 60/527,167
PRIOR PELICATION NUMBER: US 60/527,167
PRIOR PILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/601,665
PRIOR APPLICATION NUMBER: US 60/601,665
PRIOR PILING DATE: 2004-06-13
PRIOR FILING DATE: 2004-06-13
PRIOR FILING DATE: 2004-08-13
PRIOR FILING DATE: 2004-10-14
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PATENT VERSION 3:3
SOFTWARE: PATENT VERSION 3:3
LENGTH: 119
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                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic US-11-004-590-340
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                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial
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ORGANISM: Artificial
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US-11-004-590-348
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Publication No. US20060008883A1;
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan;
APPLICANT: Desjarlais, John R.;
APPLICANT: Hammond, Phillip W.;
TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
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100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                 Length 119;
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100.0%; Score 124; DB 7;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0;
    PRIOR FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: US 60/581,613
PRIOR PILING DATE: 2004-06-21
PRIOR PLING DATE: 2004-06-31
PRIOR PILING DATE: 2004-08-13
PRIOR FILING DATE: 2004-08-13
PRIOR FILING DATE: 2004-10-14
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin version 3.3
SEQ ID NO 237
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                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-590-237
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US-11-004-590-340
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Search completed: April 25, 2006, 07:10:02 Job time : 16.2044 secs
           1 OVOLORSGPGLVKPSQTLSLTCTVS 25
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Sequence 348, Application US/11004590

Publication No. US2006000883A1

GENERAL INFORMATION:

APPLICANT: Lazar, Gregory Alan

APPLICANT: Desjarlais, John R.

APPLICANT: Desjarlais, John R.

APPLICANT: Hammond, Phillip W.

TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING

TITLE OF INVENTION: CONYENT AND COMPOSITIONS THEREOF

FILE REFERENCE: 185832/US/5

CURRENT APPLICATION NUMBER: US 60/527,167

PRIOR PLILNG DATE: 2004-12-03

PRIOR PLILNG DATE: 2004-06-21

PRIOR PLILNG DATE: 2004-06-21

PRIOR PLILNG DATE: 2004-06-31

PRIOR PLILNG DATE: 2004-06-13

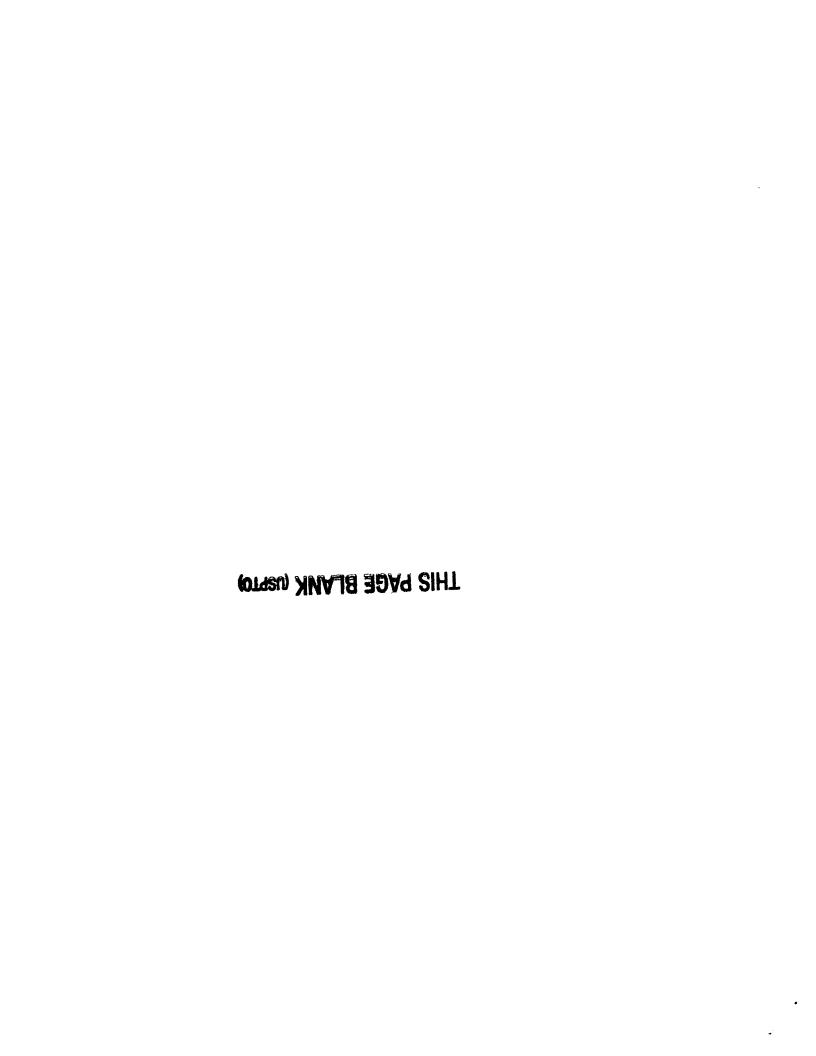
PRIOR PLILNG DATE: 2004-10-14

NUMBER OF SEQ ID NOS: 458

SEQ ID NO 348

LANGTH: 119

LENGTH: 119
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APPLICANT: Desjarlais, John R.
APPLICANT: Hammond, Phillip W.
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: 2004-12-03
CURRENT APPLICATION NUMBER: US 60/527,167
FRIOR PLILING DATE: 2004-06-21
FRIOR APPLICATION NUMBER: US 60/601,665
FRIOR APPLICATION NUMBER: US 60/601,665
FRIOR APPLICATION NUMBER: US 60/619,483
FRIOR FILING DATE: 2004-10-14
SPRIOR FILING DATE: 2004-10-14
SPRIOR FILING DATE: 2004-10-13
SPRIOR FILING DATE: 2004-10-3
SPRIOR FILING DATE: 2004-10-14
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100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels (
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Best Local Similarity 100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
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GOTHER INFORMATION: Synthetic
US-11-004-590-352
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US-11-004-590-352
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Copyright (c) 1993 - 2006 Blocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human	_		_	_	Human	Ady31516 Human ant	Ady31483 Human ant	Ady31489 Human ant	Human	Adz07629 Mouse 3A6	Aar87049 Human gro	_	Adx27037 Human gro	Ady31384 Human ant	Human	Human	Ady31402 Human ant	Human	Human	Ady31357 Human ant	Aeb13673 Human ant	Adu87725 Human hea	Aec20858 Human var
ΙD	ADQ92397	ADQ80586	ADQ90699	ADY31507	ADY31531	ADY31534	ADY31516	ADY31483	ADY31489	ADY31540	ADZ07629	AAR87049	AAE19691	ADX27037	ADY31384	ADY31351	ADY31399	ADY31402	ADY31408	ADY31375	ADY31357	AEB13673	ADU87725	AEC20858
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Length	25	25	25	25	25	25	25	25	25		29	30	30	30	30	30	30	30	30	30	30	30	44	28
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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ALIGNMENTS

Tumour necrosis factor alpha; TNF-alpha mediated disease;

KW sepsis; autoimmune disease; rheumatoid arthritis; inflammatory disease;

KW neurodegenerative disease; malignancy; TNF-secreting tumour;

KW neurodegenerative disease; malignancy; TNF-secreting tumour;

Alcohol-induced hepatitis; psoriasis; psoriatic arthritis;

KW wegener's granulomatosis; ankylosing spondylitis; heart failure;

KW wegener's granulomatosis; ankylosing spondylitis; heart failure;

KW wegener's granulomatosis; hepatitis C infection; Kawasaki's pathology;

KW Refsum's disease; ataxia; telangiectasis; Alzheimer's disease;

KW pown's syndrome; Parkinson's disease; leukaemisi myelodyspastic syndrome;

KW pypokinetic movement disorder; drug induced movement disorder;

KW pypokinetic movement disorder; drug induced movement disorder;

KW crohn's disease; ulcerative colitis; amyotrophic lateral selerosis;

KW multiple sclerosis; Grave's disease; diabetes mellitus; atherosclerosis;

KW human; heavy chain variable region; VH; FR; framework region. ğ Huse Marquis D, ADQ92397 standard; peptide; 25 AA. 08-JAN-2003; 2003US-00338627. 08-JAN-2003; 2003US-00338627. Watkins JD, Vasserot AP, 23-SEP-2004 (first entry) Human hul FRH1 peptide. (WATK/) WATKINS J D. (VASS/) VASSEROT A P. (MARQ/) MARQUIS D. (HUSE/) HUSE W D. US2004131613-A1. Homo sapiens. 08-JUL-2004. ADQ92397; RESULT 1 ADQ92397

WPI; 2004-524894/50. N-PSDB; ADQ92401. New composition comprising a tumor necrosis factor alpha (TNF-alpha)

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binding polypeptides and their encoding polymucleotides. The invention is useful for treating TNF-alpha mediated disease such as sepsis, an automame disease, theumatory diseases, an automame disease, malignant pathologies involving TNF-secreting tumours, alcohol-induced hepatitis, inflammatory diseases, natured according to tumours, alcohol-induced hepatitis, psoriasis, psoriatic arthitis, wegener; s granulomatosis, anxivosing spondylitis, heart failure, reperfusion injury, chronic obstructive pulmonary disease, pulmonary of fibrosis, hepatitis C infection, Kawasaki's pathology, Refsum's disease, cataxia, telangisctasia, Alzheimer's disease, pown's syndrome, Parkinson's disease, leukaemias (acute, chronic myelocytic, chronic lymphocytic and/or myelodyspastic syndrome). Iymphomas (Hodgkin's, non-Hodgkin's and Surkitt's syndrome), hypokinetic movement disorders, crohn's disease, ulcerative colitis, amyotrophic convenent disorders, crohn's disease, ulcerative colitis, amyotrophic collectes, multiple sclerosis, Grave's disease, diabetes collitis, and infectious diseases. The invention is also useful in antibody therapy. The present sequence is human hul framework sub-region of heavy chain variable (VH) cregion (FRH) peptide. This sequence is used in the invention.
                                                                                                                                                                                                                              present invention relates to tumour necrosis factor alpha (TNF-alpha)
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binding molecule, useful for treating a TNF-alpha mediated disease such as sepsis, an autoimmune disease, rheumatoid arthritis, and neurodegenerative diseases.
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100.0%; Pred. No. 4.7e-10;
tive 0; Mismatches 0; Indels
                                                                                                                                                     Disclosure; SEQ ID NO 65; 60pp; English.
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(HUSE/)
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Gaps

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The invention relates to a composition which comprises a TNP-alpha binding molecule having sequence of complementarity determining region (CDRJ) in 1944t chain variable region (CDRJ) and sequence of CDR in composition is useful in the neavy chain variable region (CDRJ). 3 and sequence of CDR in chart chain variable region (CDRJ). The composition is useful in the treatment of TNP-alpha mediated diseases. TNP-alpha binding molecule is useful for treating sepsis, autoimmune disease, rhematoola arthritis, allery, multiple sclerosis, systemic lupus erythematosus, scleroderma, diabetes mellitus, cachexia, acute and chronic parasitic and/or infectious diseases, sarcoidosis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, diseaninated intravascular coagulation, parkinson's disease, Alzheimer's disease, Down's syndrome, psorlasis, anthony spondylitis, Wegener's granulomatosis, idiopathic pulmonary fibrosis, asthma, graft-versus-host disease, or leukemia. TNF-alpha binding molecule is useful in diagnostic methods for detecting TNF-alpha in parients known to be or suspected of having TNF-alpha-mediated disease. TNF-alpha binding molecule is useful in immunoassays for epresents the amino acid sequence of a human heavy chain framework
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; angiogenic disorder; immunological disorder; anti-VBGF antibody; antibody; heavy chain; FR1. anti vascular endothelial cell growth factor antibody;
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                                                                                               Composition useful for treating diseases such as leukemia, asthma, rheumatoid arthritis, Alzheimer's disease, psoriasis or multiple sclerosis, comprises TNF-alpha binding molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 123; DB 8; Length 25; 100.0%; Pred. No. 4.7e-10; ive 0; Mismatches 0; Indels
Vasserot AP, Marquis D, Huse WD;
                                                                                                                                                                                  Disclosure; SEQ ID NO 65; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVESGGLVQPGGSLRLSCAAS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ90699 standard; peptide; 25 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-2003; 2003US-0442484P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                         WPI; 2004-516978/49.
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Best Local Similarity
                                                            N-PSDB, ADQ80590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004065417-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Нощо варіелв
  Watkins JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ90699;
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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.

WPI; 2005-180802/19.

Disclosure; SEQ ID NO 339; 179pp; English

The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework

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DNA library; humanized antibody, antibody engineering; heavy chain.
                                                                                                                                                                                                                                           Human antibody heavy chain framework peptide - SEQ ID 339.
                                                                                                                                                                                                                                                                                      20-AUG-2004; 2004US-00923068
                                                                                                                                                                                                                                                                                              22-AUG-2003; 2003US-0497213P.
13-OCT-2003; 2003US-0510741P.
                                                                                                                                                                                                                                                                                                            (MEDI-) MEDIMMUNE INC
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                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                           ADY31507;
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                                                                                                                                                                                                         RESULT 4
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Human antibody heavy chain framework peptide - SEQ ID 363.

(first entry)

05-MAY-2005

ADY31531;

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antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid the method described above has a substitution of at least one amino acid position with a different amino acid, where the different amino acid is the amino acid found at the corresponding FR position of a human subgroup (FVRI) and/or HVR2 amino acid sequence that has a hypervariable region. It (HVRI) and/or HVR2 amino acid sequence of the variable domain.

CHARI) and/or HVR2 amino acid sequence of the variable domain.

CHARI) and/or antigen binding fragment variable domain.

CHARI) and/or antigen binding fragment. The antibody and antigen binding fragment. The antibody and antigen binding fragments in antibody and antigen immunomodulatory activities, and can be used in antibody therapy. The methods and compositions of the present invention are useful for methods and compositions of the present invention are useful for the previous or antifered antifoning fragments in cell culture, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         particular for improving the yield of recombinant antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and inflammatory, andjogenic and immunological disorders. The present sequence represents a heavy chain FR1 peptide of an anti-VEGF (vascular endothelial cell growth factor) antibody, which is used in the exemplification of the present invention.
                                                                          Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.
                                                                                                                                                                                                                                                                                                                                                                   present invention describes a method for producing an antibody or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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100.0%; Pred. No. 4.7e-10;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                          Claim 15; SEQ ID NO 3; 161pp; English.
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Best Local Similarity 100.0
Matches 25; Conservative
WPI; 2004-562149/54.
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1 EVQLVESGGGLVQPGGSLRLSCAAS 1 EVQLVESGGGLVQPGGSLRLSCAAS

ADY31531 standard; peptide; 25 AA.

RESULT 5 ADY31531 ID ADY3

Match 100.0%; Score 123; DB 9; Local Similarity 100.0%; Pred. No. 4.7e-10; les 25; Conservative 0; Mismatches 0;

Sequence 25 AA;

peptide.

Query Match

Matches

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Length 25;

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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
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DNA library; humanized antibody; antibody engineering; heavy chain.
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                                                                                                                                                                     US2005042664-A1
                                                                                              Homo sapiens
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(first entry)

Sequence 25 AA;

Damschroder M;

Dall-Acqua W,

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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA library; humanized antibody; antibody engineering; heavy chain.
              DNA library; humanized antibody; antibody engineering; heavy chain.
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; Pred. No. 4.7e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human antibody heavy chain framework peptide
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13-OCT-2003; 2003US-0510741P.
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13-OCT-2003; 2003US-0510741P.
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                                                                              US2005042664-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 AA;
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                                                 Homo sapiens
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Best Local 8
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                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                     DNA library; humanized antibody; antibody engineering; heavy chain.
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                  Length 25;
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                                               Indels
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Score 123; Db 5;
No. 4.7e-10;
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Pred. No. 4.7e-10;
         Mismatches
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13-OCT-2003; 2003US-0510741P.
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                                                                                                                                                                                                                                                        (first entry)
    Query Match
Best Local Similarity 100...
Best Local 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Conservative
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Best Local Similarity
Matches 25; Conserv
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ADY31516

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Length 25;

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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
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                                                                                                     The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework
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                                                                                                                                                                                                                                                                                           Length 25;
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100.0%; Pred. No. 4.7e-10;
ive 0; Mismatches 0;
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                                                                         Disclosure; SEQ ID NO 315; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                              1 EVQLVESGGGLVQPGGSLRLSCAAS 25
                                                                                                                                                                                                                                                                                                                                                                                     Damschroder M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADY31489 standard; peptide; 25
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                                                                                                                                                                                                                                                                                                                              25; Conservative
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Matches 25; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                           Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                             Best Loca
Matches
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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                           DNA library; humanized antibody; antibody engineering; heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
                                                                                                                                                                                                                                                                 Human antibody heavy chain framework peptide - SEQ ID 372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 123; DB 9;
Pred. No. 4.7e-10;
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                                                                                                                                          ADY31540 standard; peptide; 25 AA
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100.0%; Pr
cive 0;
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13-OCT-2003; 2003US-0510741P.
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Humanised antibody; interleukin-5; IL-5; recombinant antibody; antibody engineering; monoclonal antibody; MAb; 39D10; CDR; complementarity determining region; heavy chain; framework; eosinophilia;

allergy; asthma

Homo sapiens W09535375-A1 28-DEC-1995.

Human group III heavy chain framework 1.

(first entry

25-JUN-1996

AAR87049;

AAR87049 standard; peptide; 30 AA

RESULT 12

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The invention relates to binding molecules (SEQ ID Nos 2 and 3) capable of binding to human NgGA polypeptide (SEQ ID No: 5), human NiG cof binding to human NGGA polypeptide (SEQ ID NO: 7), human NiG-D20 polypeptide (SEQ ID NO: 24), or human NGGA342-357 (SEQ ID NO: 6) all given in the specification, with a dissociation comprises a first antigen binding site comprising in sequence the hypervariable regions CDR-H1, CDR-H2, and CDR-H3, where each of the hypervariable regions CDR-H1, CDR-H2, and CDR-H3, where each of the hypervariable regions CDR-H1, CDR-L3, where each of the hypervariable regions CDR-H1, DAG (SEQ ID NO: 10) all given in the specification, and a second antigen binding site comprising in sequence the hypervariable comprises of the normal sequence (SEQ ID NO: 12), and CDR-H1-3A6 (SEQ ID NO: 10) all given in the specification, and a second antigen binding site comprising in sequence the hypervariable cregions are at least 50% homologous to their equivalent hypervariable cregions are at least 50% homologous to their equivalent hypervariable cregions are at least 50% homologous to their equivalent hypervariable cregions are at least 50% homologous to their equivalent hypervariable cregions are at least 50% homologous to their equivalent hypervariable cregions are at least 50% homologous to their equivalent hypervariable cregions are: (i) polymucleotide sequences encoding the binding molecules above, (ii) polymucleotide sequences encoding the binding molecules above, (ii) polymucleotide sequences encoding the binding molecule in association system or its part is present in a compatible host cell comprising the expression system or its part is present in a compatible host cell comprising the expression system or its part is present in a compatible host cell comprising the expression system or its part is present in a compatible host cell comprising the expression system or its part is present in a compatible of province of nerve repair. They are also useful in the treatment of various cell seases as for th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          retinopathy, age-related macular degeneration, or pathologic myopia. This sequence represents the N-terminal sequence of the heavy chain of mouse 3A6 antibody as determined by sequence degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New binding molecule capable of binding to human NogoA polypeptide, human NiG-D20, or human NogoA342-357, useful for treating nerve repair, Alzheimer's disease, Parkinson's disease, or amyotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurodegenerative diseases including Alzheimer's disease, Parkinson's
disease, or amyotrophic lateral sclerosis. The binding molecules amy also
be used for treating degenerative ocular disorders including diabetic
ocular disease; diabetic retinopathy; age related macular degeneration;
                     myopia, cns-gen, neuroprotective, nootropic, antiparkinsonian,
antidiabetic, ophthalmological; 3A6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vitaliti A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schwab ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 30; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mir AK,
                                                                                                                                                                                                                                                            17-SEP-2004; 2004WO-EP010489.
                                                                                                                                                                                                                                                                                                               19-SEP-2003; 2003GB-00021997.
                                                                                                                                                                                                                                                                                                                                                             (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS PHARMA GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frentzel S,
                                                                                                                                                                                                                                                                                                                                                                                                                     (UYZU-) UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-242564/25
                                                                                                                                                         WO2005028508-A2.
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                                                                                                      Mus musculus
                                                                                                                                                                                                            31-MAR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sclerosis
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Human; tumour necrosis factor 40; TNF40; osteopathic; cardiant; CDR; complementarity determining region; rheumatoid; osteo-arthritis; sepsis; congestive heart failure; shock; tissue transplant; tuberculosis; AIDS; Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome; cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis; inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;
                                                                                                                                                             Human group 3 consensus peptide #1.
                                    AAE19691 standard; peptide; 30 AA
                                                                                                                    31-MAY-2002 (first entry)
                                                                               AAE19691;
RESULT 13
                 AAE19691
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                                                                                                                                                                                   100.0%; Score 123; DB 9; Length 29; 100.0%; Pred. No. 5.4e-10; ive 0; Mismatches 0; Indels
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1 EVQLVESGGGLVQPGGSLRLSCAAS 25 EVQLVESGGGLVQPGGSLRLSCAAS 25

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25; Conservative

Best Local Similarity Matches 25; Conserv

Query Match

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Gaps

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Length 30; Indels

100.0%; Score 123; DB 2; 100.0%; Pred. No. 5.6e-10; iive 0; Mismatches 0;

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Local Similairy nes 25; Conservative

Sequence 30 AA;

Query Match Matches

framework

Pramework regions (AAR87049-52) of human group III (gp3) germ line antibody heavy chain showed homology to corresponding regions (AAR87053-56, respectively) of the rat anti-human interleukin-5 monoclonal antibody 39D10 heavy chain (see AAR87039). This homology was utilised in the prodn. of a humanised 39D10 VH (AAR87058) in which rat 39D10 VH complementarity determining regions were grafted into the human gp3

Anti-human IL-5 recombinant antibody - useful for preventing or reducing eosinophilia and for treating certain allergic diseases, esp. asthma.

Example 3; Fig 4; 69pp; English

(CLLT) CELLTECH THERAPEUTICS LTD.

95WO-GB001411. 94GB-00012230.

16-JUN-1995; 17-JUN-1994; Bodmer MW, Athwal DS,

Emtage JS,

WPI; 1996-058412/06.

Thomas K;

Mclaughlin J,

King DJ;

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The invention relates to a novel method for preparing an antibody with a cheavy and light chain comprising fermenting a cell mixture, where the calls are capable of expressing the light and heavy chain, separating the cells are capable of expressing the light and heavy chain, separating the cells from the supernatant to form a cell pellet, allowing the pellet to stand for a hold time, extracting the cell pellet and producing the pellet to common the cell pellet and producing the TNF common necrosis factor) alpha antibody fragment or its dimer or adduct. The antibody of the invention demonstrates antiarthritic, antirheumatic, gastrointestinal-gen. and antiinflammatory activities and may be useful compacted to the treatment of rheumatoid arthritis or an inflammatory bowel disease, such as crohn's disease. Currently used anti-TNF-alpha monoclonal.

CC antibodies, such as infliximab and etanercept, have limited success in the treatment of disease since they must be administered frequently or intravenously. Furthermore, both of these molecules comprise large contraints and as such are difficult and expensive to manufacture. The proteins and as such are difficult and expensive to manufacture. The current sequence is that of a human group 3 consensus heavy chain construct antibody targeted to TNF-alpha.
                                                                                                                                                                                                                                                                                                                                                                                Preparing a tumor necrosis factor-alpha antibody having a heavy and light chain comprises fermenting a cell mixture, forming a cell pellet and allowing the pellet to stand for a hold time.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA library; humanized antibody; antibody engineering; heavy chain.
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100.0%; Pred. No. 5.6e-10;
ive 0; Mismatches 0;
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                                                                                  29-JUL-2004; 2004WO-IB002529
                                                                                                                                               08-AUG-2003; 2003US-0493740P
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Matches 25; Conservative
                                                                                                                                                                                                           (PHAA ) PHARMACIA CORP
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                               17-FEB-2005.
                                                                                                                                                                                                                                                                          Banerjee A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an antibody molecule having specificity for human tumour necrosis factor-alpha (TNFalpha) comprising a heavy or light chain. The antibody or the compound comprising the antibody is useful for treating or manufacturing a medicament for treating a pathology mediated by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha mediated diseases which can be treated by the antibody include sepsia. Congestive conferences and the sepsia congestive diseases which can be treated by the antibody include sepsia. Congestive diseases syndrome, acquired immunodeficiency syndrome (AlDS), allergies, psoriasis, tuberculosis, inflammatory bone disorders, blood coagulation disorders, bronn's disease and autoimmune diseases, such as thyroiditis. The antibodies may also be used to reduce the side effects associated with TNFalpha generation during neoplasty therapy, to eliminate or reduce shock-related symptom associated with the treatment or prevention of great rejection by use of an anti-lymphocyte antibody, for treating multice organ failure, or in the diagnosis and imaging of disease states involving elevated levels of TNF alpha. The present sequence is human involved the control of the control
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibody specific for human tumor necrosis factor (TNF)-alpha, useful for treating TNF-alpha-mediated diseases, e.g. congestive heart failure, septic or endotoxic shock, cachexia, adult respiratory distress syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human group 3 consensus heavy chain framework region peptide - SEQ 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 involving elevated levels of TNF alpha. The present sequence is human group 3 consensus peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody, antiarthritic; antirheumatic; gastrointestinal-gen.; antiinflammatory; rheumatoid arthritis; musculoskeletal disease; inflammatory bowel disease; gastrointestinal disease; inflammation; Crohns disease; inmune disorder; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
      neoplasty therapy; immunomodulator; vulnerary; graft rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Weir ANC, Popplewell AG, Chapman AP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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100.0%; Pred. No. 5.6e-10;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 2; 119pp; English
                                                                                                                                                                                                                                                       05-JUN-2001; 2001WO-GB002477.
                                                                                                                                                                                                                                                                                                                 06-JUN-2000; 2000GB-00013810.
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                                                                                                                                                                                                                                                                                                                                                                             (CELL-) CELLTECH R & D LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Athwal DS, Brown DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-216732/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30 AA;
                                                                                                                                  WO200194585-A1
                                                                         Homo sapiens.
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                                                                                                                                                                                              13-DEC-2001.
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ADX27037;

RESULT 14

Query Match

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Gaps

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Indels

Length 30;

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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
                                                                                                                                                                                                                  The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework peptide.
                                                                                                                                                                        Disclosure; SEQ ID NO 216; 179pp; English.
Wu H, Dall-Acqua W, Damschroder M;
                                    WPI; 2005-180802/19.
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ö 100.0%; Score 123; DB 9; Length 30; 100.0%; Pred. No. 5.6e-10; tive 0; Mismatches 0; Indels 1 EVQLVESGGGLVQPGGSLRLSCAAS 25 1 EVQLVESGGGLVQPGGSLRLSCAAS 25 Query Match Best Local Similarity 100.0 Matches 25; Conservative ઠે 셤

Sequence 30 AA;

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Gaps

Search completed: April 25, 2006, 06:15:08 Job time : 134.491 secs

Tue Apr 25 08:25:48 2006

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

Run on:

April 25, 2006, 06:15:41; Search time 21.2264 Seconds (without alignments) 113.322 Million cell updates/sec

US-10-764-428-3 123 Title: Perfect score:

1 EVQLVESGGGLVQPGGSLRLSCAAS 25 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Ig heavy	Ig heavy chain	Ig heavy	Ig heavy	5 Ig heavy	Ig heavy chain	Ig heavy	. Ig heavy	Ig heavy	Ig heavy	Ig heavy che	Ig variable reg	Ig heavy cha																
	a	826890	846462	PL0121	\$26894	S2954	826934	PL0123	S26891	826896	826933	826925	826926	836280	817079	821980	836259	A34964	831121	GIHUTE	831107	M3HUBW	826794	831509	820775	830531	831587	137781	822657	444
	BB	~	~	7	N	~	~	7	~	~	~	8	~	~	7	~	~	7	7	-	~	٦	~	~	7	7	~	N	~	,
	Length	97	97	86	98	98	98	86	98	98	98	100	100	114	117	117	117	117	118	119	119	120	123	123	124	125	136	139	140	
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
	Score	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	
	Regult No.	-	10	ı	4	· LO	•	7	•	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23		25	26	27	28	

5	heavy chain heavy chain	heavy o	heavy chain	heavy	heavy	heavy	heavy	neavy	neavy	neavy
137780 JL0048	B28966 C34964	S26889 S54856	PL0122	H3HUTL	ATHUTU	H3HU26	A45953	B34964	МЗНОРМ	D36005
147 2		98			116 1	117 1				119 2
100.0		97.6								
123	122	120	120	120	120	120	120	120	120	120
30 31	332	6. E.	36	34 38	39	4 4 0 1	42	43	44	45

ALIGNMENTS

RESULT 1 S26890 S26890 Ig heavy chain V region (DP-48) - human (fragment) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 C; Accession: S26890 C; Mol. Biol. 227, 776-798, 1992 A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V A; Reference number: S26885; MUID: 93021117; PMID: 1404388
A; Status: preliminary A; Status: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-97 <tom> A; Cross-references: UNIPARC; UPI00001138FA; EMBL; Z12348; NID: 932916; PIDN: CAA78218.1; PIC C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F; 15-97/Domain: immunoglobulin homology <imm></imm></tom>
Query Match 100.0%; Score 123; DB 2; Length 97; Best Local Similarity 100.0%; Pred. No. 3.7e-10; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

22 1 EVQLVESGGGLVQPGGSLRLSCAAS

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pheavy chain V region (YAC-5) - human C;Gpacies: Homo sapiens (man) C;Date: 20-Peb-1995 #sequence_revision 20-Peb-1995 #text_change 23-Jul-1999 C;Accession: S4662 R;Oook, G.P.; Tominson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Win Nature Genet. 7, 162-168, 1994 A;Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telo: A,Reference number: S46462 A,Reference number: S46462 A,Status: preliminary A,Status: preliminary A,Residues: 1-97 <COO>

Ajcose-references: UNIPARC:UP100001165D9; EMBL:Z27504; NID:g505430; PIDN:CAA81824.1; P. C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin T region; immunoglobulin P:15-97/Domain: immunoglobulin homology < IMM>

ö Length 97; Indels Query Match 100.0%; Score 123; DB 2; Best Local Similarity 100.0%; Pred. No. 3.7e-10; Matches 25; Conservative 0; Mismatches 0;

1 EVQLVESGGGLVQPGGSLRLSCAAS 25

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Gaps

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Gaps

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Indels

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A;Cross-references: UNIPARC:UP10000116412; EMBL:Z17392; NID:g32840; PIDN:CAA78996.1; PID C;Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology c!Keywords: heterotetramer; immunoglobulin homology cIMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region (DP-59) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 526934
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: $26885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UP10000116415; EMBL:Z12359; NID:g32937; PIDN:CAA78229.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V-III region (TD-Vr) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Jace: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: P£00123; S26897
R;Bird, J; Galili, N.; Link, M.; Stites, D.; Sklar, J.
R;Bird, J; Galili, N.; Link, M.; Stites, D.; Sklar, J.
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A;Reference number: P£0116; MUID:88286083; PMID:2840480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Rodecule type: mRNA
A,Residues: 1-98 «BIR»
A,Cross-references: UNIPARC:UPI0000116413
A,Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A,Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement f
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A,Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A,Reference number: $26885; WUID:93021117; PMID:1404388
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                                                                                                                                                                                                                                                                        ; Score 123; DB 2;
; Pred. No. 3.8e-10;
0; Mismatches 0;
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100.0%; Score 123; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                            ch 100.0%;
1 Similarity 100.0%;
25; Conservative 0
        A; Molecule type: DNA
A; Residues: 1-98 <TOM>
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A;Residues: 1-98 <TOM>
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Best Local &
                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                   In heavy chain V-III region (TD-Vp) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: D, -interpretation (man)
C; Species: D, -interpretation (man)
C; State (man)
C; Stat
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326894
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Accession: S26894
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Moll. Biol. 227, 776-798; 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups (A). Reference number: S26885; MUID:93021117; PMID:1404388
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Ig heavy chain V region (COS 6) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29545
R;Tomlinson, M; Walter, G; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Reference number: S29543
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100.0%; Pred. No. 3.8e-10;
tive 0; Mismatches 0;
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1 EVQLVESGGGLVQPGGSLRLSCAAS
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Best Local Similarity 100.
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Best Local Similarity
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A; Residues: 1-98 <TOM>
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A;Status: preliminary
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26933
A;Status: prellminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UP1000011640D; EMBL:Z12340; NID:932902; PIDN:CAA78210.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S26925 "Courselon LU-NOV-1995 #text_change 23-Jul-1999
R; Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A; Reference number: S26885; MUID: 93021117; PMID: 1404388
A; Accession: S26925
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A;Residues: 1.100 <TOM>
A;Cross-references: UNIPARC:UPI0000116407; EMBL:Z12332; NID:g32883; PIDN:CAA78202.1; PI:
A;Cross-references: UNIPARC:UPI0000116407; immunoglobulin v region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
P;15-100/Domain: immunoglobulin homology <IMM>
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26926
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region (DP-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 123; DB 2;
Pred. No. 3.8e-10;
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100.0%; Pred. No. 3.8e-10;
trive 0; Mismatches 0;
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100.0%; Score 123; D
Best Local Similarity 100.0%; Pred. No. 3.8
Matches 25; Conservative 0; Mismatches
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Best Local Similarity 100.0
Matches 25; Conservative
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826891
Ig heavy chain V region (DP-58) - human (fragment)
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Species: Date: 22-Nov-1933 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 826891
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Nol. Biol. 227, 776-798, 1992
A;Tile: The repertodre of human germline V(H) sequences reveals about fifty groups of V, Reference number: 8268891
A;Reference number: 8268891
A;Reference number: 826891
A;Reference number: 826891
A;References: UNIPARC:UP10000116414; EMBL:Z12358; NID:g32935; PIDN:CAA78228.1; PIC C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999

A; Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A; Accession: Sz6896

A; Accession: S26896

A; Accession: Sz6896

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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26933
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100.0%; Score 123; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                 Length 98
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; Pred. No. 3.8e-10;
0; Mismatches 0;
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1. Similarity 100.0%; Pred. No. 3.8e-10;
25; Conservative 0; Mismatches 0:
                                       P;49-65/Region: complementarity-determining 2
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Best Local Similarity 100.0%;
Matches 25; Conservative 0
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Best Local
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826933
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Search completed: April 25, 2006, 06:26:12 Job time : 22.2264 secs
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                                                                                                                                            RESULT 13
836280
Ig Heavy chain V region (clone alpha-POG1-A3) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: 336280
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: 336256; MUID:93178448; PMID:7679990
A;Accession: 536280
A;Accession: 536280
A;Accession: WINPARC:QUIDE6; UNIPARC:UPIO000176DIB; EMBL:218822
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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S17079
Glay chain V-gene (clone HHG19) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 20-Peb-1995 #sequence revision 20-Peb-1995 #text_change 23-Jul-1999
C;Accession: S60299; S17079
C;Accession: Lett. 34, S7-52, 1992
Immunol. Lett. 34, S7-52, 1992
A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm A;Reference number: S60295; MUD:93122853; PMID:1282498
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A;Molecule type: DNA
A;Cross-references: UNIPARC:UPI0000115FF4; EMBL:X62128; NID:g38340; PIDN:CAA44059.1; PID
A;Note: the authors did not translate the codons for residues 6, 52, 54, 68, 69, 71, 72, C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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(5,5pecies; Homo sapiens (man)
(5,5pecies; Homo sapiens (man)
(5,5pecies; 20-Fbb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
(5,Accession: 860295; 821980
(7,Roreperst, R.; Flachert, U.; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm
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100.0%; Score 123; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 123; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.4e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-117 <KU2>
A;Cross-references: UNIPARC:UP10000115FP6; EMBL:X62130; NID:g38344; PIDN:CAA44061.1; PID
C;Genetics:
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                                                                                                                                                                                                                                                                                                      Length 117;
                                                                                                                                                                         A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                     0; Indels
A; Reference number: S60295; MUID: 93122853; PMID: 1282498
                                                                                                                                                                                                                                                                                                 ch 100.0%; Score 123; DB 2; Il Similarity 100.0%; Pred. No. 4.4e-10; 25; Conservative 0; Mismatches 0;
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Best Local Similarity
                          A; Accession: S60295
A; Status: preliminary
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(Fragment).
Homo saptens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probled Section Section 1. Pubmed-155592;

A Makiya R., Stigbrand T.;

Makiya R., Stigbrand T.;

Makiya R., Stigbrand T.;

Makiya R., Stigbrand T.;

I placental alkaline phosphatase has a binding site for the human immunoglobulin-G Fc portion.";

Bur. J. Blochem. 205:341-345(1992).

Bur. J. Blochem. 205:341-345(1992).

R FMB; AP035042; AAD56278.1; -; mRNA.

RR; C31205; S21205.

RR; PRO173; 1106.

RR; C9UL72; 1-118.

InterPro; IPR003106; Ig-like.

RR; C9UL72; IPR003106; Ig-like.

RRRT; SM0406; IGV; 1.

PRESITE; PSS0835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLECTIDE SEQUENCE.
MEDLINE-98271139; PubMed-9614934; DOI=10.1006/clin.1998.4531;
MRDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531;
MR X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
QG61n78
QG62vx0
QG62vx0
QO98xa4
QG9my2
P01775
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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                                                            44 MOUSE
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HV20 MOUSE
HV21 MOUSE
HV19 MOUSE
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HV23 MOUSE
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OUT.2 :
01-MAY-2000 (TYEMBLYE) 13, 01-MAY-2000 (TYEMBLYE) 13, 101-MY-2000 (TYEMBLYE) 13, 101-OCT-2003 (TYEMBLYE): 25, 11
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Q9UL91 HUMAN
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                                  GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Database :

2166443 segs, 705528306 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

1 EVQLVESGGGLVQPGGSLRLSCAAS 25

US-10-764-428-3 123

Perfect score:

Sequence:

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O725M1_HUMAN O6GMW7_HUMAN Q96K68_HUMAN Q65ZC9_HUMAN HV57_MOUSB

HV3F HÜMAN Q9ULBB HUMAN Q6MZU6_HUMAN

1115 131 464 470

Q6N096 HUMAN Q8N4Y9_HUMAN Q96BB9_HUMAN

HV3R HUMAN HV3C HUMAN HV3O HUMAN HV3M HUMAN

HV3S_HUMAN HV54_MOUSE HV55_MOUSE Q5F2I8_MOUSE

OGPIBI HUMAN OGMZVG HUMAN OGGWZZ HUMAN HVOS CARAU

Q9UL72_HUMAN Q9UL91_HUMAN HV3P_HUMAN HV3E_HUMAN

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21-JTL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
19 heavy chain V-III region TEI.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                           nouso sagreis, netazona, Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryote; Metazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                          Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
Diamond B.;
                                                                                                                                                                                                                                                                                                   PubMed=1555592;
Makiya R., Stigbrand T.;
Maunoglobulin-G Fc portion.";
Eur. J. Blochem. 205:341-345(1992).
EMBL; AR035023; AAD56259.1; -; mRNA.
                                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                             MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
                                                                                                                                                                                                                                               "Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.";
J. Exp. Med. 174:1639-1652(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 118;
                                                                                                                                         Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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MEDLINE=74142702; PubMed=4522793;
Capra J.D., Kehoe J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig.v.
SMART; SM00406; IGv; 1.
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PIR; S21205; S21205.
PIR; S30531; S30531.
HSSP; P01783; IIGC.
SMR; Q9UL91; 1-117.
                                                    Homo sapiens (Human)
                                                                                                                    NUCLEOTIDE SECUENCE.
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                                                                                                                                                                                                                   PubMed=1660528;
                                                                                                                                                   Young D.C.;
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ID HV3P_HUMAN
AC P01777;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 04, Last sequence update)
10-MAY-2005 (Rel. 47, Last amnotation update)
1g heavy chain V-III region BRO.
1g heavy chain V-III region BRO.
Bukaryota, Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Immunochemistry 13:95-999(1976).
-|- MISCELLANEOUS: This chain was obtained from IgM isolated from the serum of a patient with malignant lymphoma of the Waldenstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
"Variable region sequences of five human immunoglobulin heavy chain
of the VH3 subgroup: definitive identification of four heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SEQUENCE.
MEDLINE=77117674; Pubmed=65324; DOI=10.1016/0019-2791(76)90271-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                 hypervariable regions.";
Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
-!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005576; C:extracellular region; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:000555; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 AA.
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PROSITE; PS50835; IG LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A02060; GIHUTE.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A02049; M3HUBW.
HSSP; P01783; 11GC.
SMR; P01766; 1-120.
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Query Match
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ID QG
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A treamber R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A tacchul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A tacchul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A popking R.F., Jordan H., Moore T., Max S.I., Mang J., Heideh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A patchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B hownstein M., Soares M.B., Bonaldon M.F., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B hosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunzarene P.H.,

A Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rhich J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Schmutz J., Myers R.M.,

Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,

Butterfield Y.S.N., Krzywinski M.I., Marra M.A.,

Rochnerztion and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB-Primary B-Cells;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                           100.0%; Score 123; DB 1; Length 120; 100.0%; Pred. No. 1.8e-09; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                120 AA; 13227 MW; D3F0428F7C2E6410 CRC64;
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
I GO; GO:0006955; P:immune response; NAS.
InterPro; IPRO0110; Ig-like.
InterPro; IPRO01596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
DOMAIN.
1 111 Ig-like.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                          478 AA
                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
                                                                                                                                                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAAS 25
                                                                                                                                                                                                                                                                                                                                                                                      Created)
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HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                          PRT;
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Interpro; IPR003599, 19-11ke.
Interpro; IPR003597, 19_C1.
Interpro; IPR003006, 19_MHC.
Interpro; IPR003596, 19_V.
Pfam; PP07654; C1-8et; 3.
                                                                                                                                                                                                              100.04;
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                                                                                                                                                                                                                                                                                                                                                     QEP181_HUMAN PRELIMINARY;
QEP181;
                                                                                                                                                                                                                            25; Conservative
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NIH MGC Project;
                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                  IGHM protein.
Name=IGHM;
                                                                                                                                                     NON TER
SEQUENCE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Robo G., Han M., Wiemann S., Submitted (AUG-2003) to the EWBL/GenBank/DDBJ databases.

RMBL BK646854; CAR45921.1; -; mRNA.

HSSP, P01842; 1AQK.

SMR, OGMZUK.
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                                                                                                                                                                                                                                                        100.0%; Score 123; DB 2; Length 478; 100.0%; Pred. No. 7.2e-09; ive 0; Mismatches 0; Indels C
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SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGC; IG; IIC; II.
PROSITE; PS00290; IG MRC; UNKNOWN 2.
SEQUENCE 478 AA; $\begin{array}{c} \begin{array}{c} \end{array}
\end{array}
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheltal protein DKFZp686L19235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 123; DB 2;
100.0%; Pred. No. 7.2e-09;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVOLVESGGGLVQPGGSLRLSCAAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNRNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE; POLGAS; AMER; GMER; GMER; GMERS; POLGAS; ISTACK; InterPro; IPR003159; IG. InterPro; IPR003159; IG. InterPro; IPR003598; IG. InterPro; IPR003598; IG. InterPro; IPR003598; IG. InterPro; IPR003596; IG. WHC. InterPro; IPR003596; IG. WHC. INTERPRO; IPR003596; IG. WHC. INTERPRO; IPR004596; IG. WHERT; SM00409; IG.; A. SMART; SM00408; IGC1; 3. SMART; SM00406; IGC1; 1.
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QGMZV6 HUMAN PRELIMINARY;
QGMZV6;
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Q6GMX2;
                                                                                                                                                                                                                                                                                                         Best_Local Similarity 100.
Matches 25; Conservative
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SEQUENCE 47
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Conservative
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54
68
84
116
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SMR; P19181; 20-116.
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                                                                      fish.";
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REGION
REGION
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                                                                                                                                   Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Butchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldow M.F., Carrinci P., Frange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Frange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Frange C.,
Brownstein M.J., Wickenan K.J., Malak J.A., Gunarane P.H.,
Raha S.S., McDley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
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                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig heavy chain V region 5A precursor.
Carassius auratus (Goldfish).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
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                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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100.0%; Pred. No. 7.4e-09;
iive 0; Mismatches 0;
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25; Conservative
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           Homo sapiens (Human).
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                                                                                               NUCLEOTIDE SEQUENCE
                                                                 NCBI_TaxID=9606;
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ID HV05_CARAU
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKPZp686C11235.
Name-DKFZp686C11235;
Name-DKFZp686C11235;
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Eusarchontoglires; Primates; Catarrhini; Hominidae;
NUCLEOTIDE SEQUENCE.
MEDLINE-88144476; PubMed=3125551;
Wilson M.R., Middleton D., Warr G.W.;
Wilson M.R., Middleton D., Warr G.W.;
"Immunoglobulin heavy chain variable region gene evolution: structure and family relationships of two genes and a pseudogene in a teleost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Decker H., Boecker M., Bandt P., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; M., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; M., Weil B., Amid C., Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640853; CR845920.1; -; mRNA.

RMBL; BX640853; CR845920.1; -; mRNA.

R HSSP; P01861; JADQ.

IN INTERPO: IPR003597; Ig.-C1.

IN INTERPO: IPR003597; Ig.-C1.

R INTERPO: IPR003597; Ig.-C1.

R INTERPO: IPR003596; Ig.-V.

R R MART; SM00409; IG.2.

SMART; SM00407; IGC1; 3.
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InterPro; IPR031596; Ig-v.
SMART; SM00406; IGv.
PR051TE; PS06135; IG LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12808 MW; 9C2279E2DF199B12 CRC64;
                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.2%; Score 122; DB 1; 96.0%; Pred. No. 2.4e-09;
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TISSUE=Small intestine;
The German cDNA Consortium;
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                      Hōmo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                               MEDLINE=78005528; PubMed=409716; Mang A.-C., Wang I.Y., Fudenberg H.H.; Mang A.-C., Wang I.Y., Pudenberg H.H.; Mang A.-C., Wang I.Y., Pudenberg H.H.; Immunoglobulin structure and genetics. Identity between variable regions of a mu and a gamma2 chain."; J. Biol. Chem. 252:7192-7199(1977).

-i. MSCELLLMREOUS: The sequences of the V regions of the heavy chains of IgM and IgG2 isolated from a single patient with biclonal gammopathy are identical. Their light chains are apparently also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=74142702; PubMed=4522793; Capra J.D., Kehoe J.M.; Capra J.D., Kehoe J.M.; Capra J.D., Kehoe J.M.; Wariable region sequences of five human immunoglobulin heavy chains of the VH3 subgroup: definitive identification of four heavy chain hypervariable regions. "1.845-848(1974).
Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
                                                                                                                                                                                                                                                                                                                            -i- SIMILARITY: Contains 1 1g-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 120; DB 1; Length 115; Pred. No. 4.6e-09;
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SMR; P01765; 2-115.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003566; Ig-v.
SMART; SM00406; IGV; 1.
PROSITE; PSS0335; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
19 heavy chain V-III region TUR.
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Ig heavy chain V-III region TIL.
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Best Local Similarity 96.09
Matches 24; Conservative
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PROTEIN SEQUENCE.
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                                                                                                                                      PROTEIN SEQUENCE.
                                                                                                  NCBI_TaxID=9606;
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P01779;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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NUMBOL-1730252;
Rapbhocat F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
Schuurman R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Myosin-reactive autoantibodies in rheumatic carditis and normal
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97.6%; Score 120; DB 2; Length 113;
Best Local Similarity 96.0%; Pred. No. 4.5e-09;
Matches 24; Conservative 1; Mismatches 0; Indels
                                                                                                    99.2%; Score 122; DB 2; Length 473; 96.0%; Pred. No. 9.9e-09;
                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                             0; Indels
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      PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 473 AA; 52121 MW; 9476RAE4COBFC447 CRC64;
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(Rel. 01, Last sequence update)
(Rel. 47, Last annotation update)
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Bur. J. Immunol. 22:247-251(1992).
EMBL; AF035024; AAD56260.1; -; mRNA.
PIR; S78486; S78486.
                                                                                                                                                                                                                                                                                                                          113 AA
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PROSITE; PS50835; IG_LIKE; 1.
                                                                                         Query Match
Best Local Similarity 96.0%
                                                                                                                                                                                                                                                                                                                        QUL90_HUMAN PRELIMINARY;
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SMR; Q9UL90; 1-113.
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P01765;
21-JUL-1986 (
21-JUL-1986 (
10-MAY-2005 (
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P01776;
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                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMES outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=93209281; PubMed=7681398;
Mariette X., Tsapla A., Erouet J.C.;
"Nucleotidic sequence analysis of the variable domains of four human monoclonal IgM with an antibody activity to myelin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constant
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Matthyssens G., Rabbitts T.H.;
Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region.";
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3D-STRUCTURE MODELING OF 20-117.

MEDILINE=866094276; PubMed=3866244.

TOYONAGA B., VSDAIKAI Y., JOINING, and constaregion agenes of the human T-cell receptor beta chain.";

Proc. Natl. Acad. Sci. U.S.A. 82:8624-8628 (1985).

- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                                                      PIR; A02062; AlHUTU.

HSSP; P01783; 1IGC.

GO; GO:0005576; C:extracellular region; NAS.

GO; GO:000823; F:antigen binding; NAS.

GO; GO:0006955; P:immune response; NAS.

INTERPRO; IRRO7110; Ig-like.

INTERPRO; IRRO03596; Ig-v.

SMART; SM00406; IGv; 1.

PROSITE; PSSO815; IG LIKE; 1.

Direct protein sequencing; Immunoglobulin domain;

Immunoglobulin V region.
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21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
19 heavy chain V-III region VH26 precursor.
Homo sapiens (Human)
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Eur. J. Immunol. 23:846-851(1993).
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P01764;
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                        PIR; A02047; H3HU26.
PDB; 1HOU; Model; H=20-117.
PDB; C0:0005876; C:extracellular region; NAS.
POS: C0:0005876; C:extracellular region; NAS.
POS: C0:0005876; P:extracellular region; NAS.
PROSTTE; PS50835; IG LIKE; 1.
PROSTTE; PS50835; IG LIKE; 1.
PROSTTE; PS50835; IG LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
-!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
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Ig-like.
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PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
DOMAIN I 112 Ig-like.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig heavy chain V-III region WAS.
Homo sapiens (Human).
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EMBL; J00236; AAAS3516.1; -; Unassigned DNA.
EMBL; M35415; AAAS8735.1; -; Genomic_DNA.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1G heavy chain V-III region POM.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE.
MEDLINE=75046755; PubMed=4139708;
Capra J.D., Kehbe J.M.;
"Structure of antibodies with shared idiotypy: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins.";
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-!- MISCRLLANBOUS: This chain was isolated from IgM with anti-gamma globulin activity.
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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during isolation).
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                                        97.6%; Score 120; DB 1; Length 117; 96.0%; Pred. No. 4.7e-09; tive 1; Mismatches 0; Indels
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117 117
117 AA; 13091 MW; 201DBF0B1B53D9BF CRC64;
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InterPro; IPR003596; Ig-v.
SMART; SM0406; IGv; 1.
PROSITE; PSS0835; IG-LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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HSSP; P01772; 2FB4.
SMR; P01774; 1-119.
                                                            Best Local Similarity
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NCBI_TaxID=9606;
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Sequence 660, App Sequence 661, App Sequence 661, App Sequence 665, App Sequence 32, App Sequence 394, App Sequence 594, App Sequence 596, App Sequence 596, App Sequence 4, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli

US-09-534-717-660 US-09-534-717-662 US-09-534-717-664 US-09-534-717-665 US-09-534-717-665 US-10-194-975-32 US-09-534-717-595 US-09-534-717-595 US-09-534-717-596 US-09-534-717-596 US-09-534-717-596 US-09-534-717-596 US-08-428-197-4 US-08-428-197-4 US-08-428-197-4 US-08-428-197-4

PCT-US93-10555-3 US-08-974-899-6 US-09-795-798-6 US-08-908-469-11

ALIGNMENTS

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CORRESPONDENCE ADDRESS:
ADDRESSE: Finnegan, Henderson, Farabow, Garrett & Dunner STREET: 1300 1 Street, N.W.
CITY: Washington
CITY: Washington
STATE: D.C.
COUNTY: USA
ZIP: 20005-3315
COMPUTER: IBM PC compatible
CURRENT APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 93401310.3
FRIOR APPLICATION NUMBER: FR 93401310.3
FRIOR APPLICATION NUMBER: FR 93401310.3
APPLICATION NUMBER: R 93 33 33 34 ATTORNEY/AGENT INPORMATION:
NAME: POLTER: Jane B.R.
REGIENATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 33,332
REFERENCE/COMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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Sequence 80, Application US/08471780C

Patent No. 5758808

GENERAL INFORMATION:

APPLICANT: Casterman, Cecile

APPLICANT: Hamers, Raymond

TITLE OF INTENTION: Immunoglobulins Devoid of Light Chains

TUTHE OF INTENTION: Immunoglobulins Devoid of Light Chains

NUMBER OF SEQUENCES: 130

CORRESPONDENCE ADDRESS:

ADDRESSER: Finnegan, Henderson, Parabow, Garrett & Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
CRIGINAL SOURCE:
CREANISM: Camelus dromedarius
US-08-471-780C-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                              April 25, 2006, 06:25:05; Search time 33.7264 Seconds (without alignments) 61.284 Million cell updates/sec
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                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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. / Gop_2 6/ptodata/1/laa/5_COMB.pep:*

. / Gop_2 6/ptodata/1/laa/6_COMB.pep:*

. / Gop_2 6/ptodata/1/laa/H_COMB.pep:*

. / Gop_2 6/ptodata/1/laa/H_COMB.pep:*

. / Gop_2 6/ptodata/1/laa/RE COMB.pep:*

. / Gop_2 6/ptodata/1/laa/RE COMB.pep:*

. / Gop_2 6/ptodata/1/laa/RE COMB.pep:*
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US-08-417-1282A-80

US-08-468-739-69

US-08-293-765A-80

US-09-293-765A-80

US-09-293-765A-80

US-09-293-765A-80

US-09-347-061-17

US-09-347-061-17

US-09-347-061-17

US-09-544-17-638

US-09-544-17-638

US-08-211-202-116

US-09-315-574-31

US-09-315-574-31

US-09-315-574-31

US-09-315-574-31

US-10-194-975-15

US-10-194-975-15
                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             572060 seqs, 82675679 residues
                                                                                                                                                                                                                1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                     Sequence 80. Application US/08467282B
; Sequence 80. Application US/08467282B
; Sequence 80. Application US/08467282B
; Patent No. 5800038B
; GENERAL INFORMATION:
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESSES: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STREET: 1300 I Street, N.W.
STREET: 12005-3315
COMPUTER: D.G.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER: RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PREADALE FORM:
MEDIUM TYPE: PLOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUNTRY: BAPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 01-3093
FILING DATE: 01-3093
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: RP 93401310.3
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: 21-AUG-1992
APPLICATION NUMBER: RP 93401310.3
FILING DATE: 202-408-4000
TELECOMMUNICATION INPERMATION:
TELEPAN: 202-408-4000
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Query Match 100.0%; Score 123; DB 1; Length 26; Best Local Similarity 100.0%; Pred. No. 2.2e-11; Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                1 EVOLVESGGGLVQPGGSLRLSCAAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAAS 25
                                                                                                       1 EVOLVESGGGLVQPGGSLRLSCAAS 25
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; Sequence 80, Application US/08471282A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARAPTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Gaps
GENERAL INFORMATION:

APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION:

NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSE: 1300 I Street, N.W.
CITY: Weshington
STREET: 1300 I Street, N.W.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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| Patent No. 5874541
| GENERAL INFORMATION:
| APPLICANT: Caeterman, Cecile
| APPLICANT: Hamers, Raymond
| TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
| NUMBER OF SEQUENCES: 130
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04958.0008-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REPERENCE/DOCKET NUMBER: 0495
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPHANE: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 80: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005-3315
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US-08-466-710C-80
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Sequence 80, Application US/09293769A

Sequence 80, Application US/09293769A

GENERAL INFORMATION:
APPLICANT: HARBES, RAYMOND
ITILE OF INVENTION: INMUNOCIOBULINS DEVOID OF LIGHT CHAINS
ITILE OF INVENTION: INMUNOCIOBULINS DEVOID OF LIGHT CHAINS
ITILE REFERENCE: 04958.0008-07000
CURRENT APPLICATION NUMBER: US/09/293,769A

CURRENT FILING DATE: 1999-04-19
FRIOR PILING DATE: 1999-04-19
FRIOR PILING DATE: 1999-06-05
FRIOR PILING DATE: 1997-10-15
FRIOR FILING DATE: 1997-06-11
FRIOR FILING DATE: 1997-06-21
FRIOR FILING DATE: 1993-05-21
FRIOR FILING DATE: 1993-05-21

FRIOR FILING DATE: 1993-05-21

SEQ ID NO 80

LENGTH: 26

MUMBER: PALENTIN VOIL 2.1

SEQ ID NO 80

LENGTH: 26

MUMBER: PALENTIN VOIL 2.1
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Pred. No. 2.2e-11;
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                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILIND DATE: 21-MAY-1993
ATTONNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REPRENCE/POCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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US-08-537-871A-4
; Sequence 4, Application US/08537871A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Camelus dromedarius
US-08-468-739C-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 25; Conservative 0
                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acide
21-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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US-09-293-769A-80
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Patent No. 6015695
GENERAL INFORMATION:
APPLICANT: Gasterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
TITLE OF INVENTION: Handerson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STREET: 100 I Street, N.W.
STREET: USA
COUNTRY: USA
ILL 20005-3315
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC LOS/MS-DOS
COMPUTER: IBM FC 
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100.0%; Score 123; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE PATENTIA Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,739C
FILING DATE: 06-JUN-1995
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,710C
                                                                                                                                                                                                                                                                    PRIOR APPLICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INPORMATION:
NAME: POCKET, Jane B.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPONE: 202-408-400
TELEPONE: 202-408-400
INPORMATION FOR SEG ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-466-710C-80
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US-08-468-739C-80
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Query Match 100.0%; Score 123; DB 1; Best Local Similarity 100.0%; Pred. No. 2.6e-11; Matches 25; Conservative 0; Mismatches 0;
                               CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DORBEN YATKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0044
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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06 JUNE-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc feature
; OTHER INFORMATION: Consensus
US-09-347-061-17
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide US-08-470-139-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-347-061-17
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                                                                   APPLICANT: Raymond HAMERS
APPLICANT: Sergle HAMERS-CASETERMAN
APPLICANT: Sergle V. M. MUYLDERMANS
APPLICANT: Leon G. J. FRENKEN
APPLICANT: Cornelis T. VERRIPS
APPLICANT: Cornelis T. VERRIPS
TITLE OF INVENTION: Production of antibodies or (functionalized)
TITLE OF INVENTION: Cragments thereof derived from heavy chain immunoglobulins
TITLE OF INVENTION: of Camelidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
NUBBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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APPLICATION NUMBER: US/08/470,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: human heavy chain framework (subgroup III)
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: Pillebury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE, MICTOSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,871A
FILING DATE: 29-JAN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATI
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COMPUTER READABLE FORM:
MEDIUM TYPE: 11.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5998586
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 25, Conservative
                                       GENERAL INFORMATION:
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US-08-470-139-17
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Sequence 17, Application US/09347061

Sequence 17, Application US/09347061

Sequence No. 6316227

GENERAL INFORMATION:

APPLICANT: Bodner, Mark

APPLICANT: Athwal, Dilject Singh

APPLICANT: Batage, John Spencer

TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies

TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies

TITLE OF INVENTION: 1999-07-02

CURRENT PILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.0

SEQ ID NO 17

LENGTH: 30
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Sequence 17, Application US/09855271

Patent No. 6734286

GENERAL INPORMATION:

APPLICANT: Bodmer, Mark W

APPLICANT: Entwal, Diljeet Singh

APPLICANT: Entwal, Diljeet Singh

APPLICANT: Entage, US/09/08

TITLE OF INVENTION Interleukin-5 Specific Recombinant Antibodies

FILE REFERENCE: CARP-0088

CURRENT APPLICATION NUMBER: US/09/0855,271

CURRENT PILING DATE: 2001-05-15

PRIOR PILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1
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Length 30;
                                                             0; Indels
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JS-09-534-717-638
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COUNTRY:
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Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                           Query Match
100.0%; Score 123; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PATENTI VETSION 3.1
SEQ ID NO 31
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
FRIOR APPLICATION NUMBER: US 60/305,111
FRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 97
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Patent No. 6881557
                                                                                                                                                                                                                                                                                                                RESULT 11
VS-10-194-975-18
Sequence 18, Application US/10194975
Patent No. 6881557
                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                ; OTHER INFORMATION: Consensus US-09-855-271-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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US-10-194-975-31
LENGTH: 30
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Sequence 638, Application US/09534717

Patent No. 6914128
GENERAL INFORMATION:
FAPLICATION Salfeld et al.
TITIE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing TITIE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing TITIE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing FILE REFERENCE: BBI-093CP
CURRENT PRILING DATE: 2000-03-24
EARLIER PILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 638
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYETEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/21,202
PILING DATE: 23-SEP-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9120252.3
PILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 25-SEP-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: A-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206312.6
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
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Sequence 116. Application US/08211202
Sequence 116. Application US/08211202
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIER, Michael;
APPLICANT: WINTER, Michael;
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies:
TITLE OF INVENTION: Combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 123; DB 2; 100.0%; Pred. No. 9.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVESGGGLVQPGGSLRLSCAAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLVESGGGLVQPGGSLRLSCAAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Homo sapiens
US-09-534-717-638
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: Illinois
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Best Local Similarity
Matches 25; Conserv
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Stephen M.J.
Anthony R.
A, Michael A.
Braydon C.
SURFACE RESIDUE VENEERING OF RODENT
ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ANIMOLICAL NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSE: Sughrue, Mion, Zinn, Macpeak & Seas STRET: 2100 Pensylvania Avenue, N.W.
CITY: Washington
CITY: Washington
COUNTRY: United States
ZIP: 20037-3202
COMPUTE: Ploppy disk
COMPUTE: HP 9000/700 Workstation
COMPUTE: Global STREET
COMPUTE: HP 9000/700 Workstation
COMPUTE: Global STREET
COMPUTE: HP 9000/700 Workstation
COMPUTE: Global STREET
COMPUTE: HP 9000/700 Workstation
COMPUTE: MANAGERISTICS:
LENGTH: 90 maino acids
TUPPEL STREET
COMPUTE: MANAGERISTICS:
LENGTH: 90 maino acids
TUPPER STREET
COMPUTE: MANAGERISTICS:
LENGTH: 90 maino acids
FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: DAVIG W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
FILLECOMMUNICATION INFORMATION:
FILLEPAK: 312-474-6300
FILLEPAK: 312-474-6448
FILLERX: 25-3856
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
FYPE: amino acids
FYPE: amino acid
FYPE: amino acid
FYPE: amino acid
FOLLOGY: Innear
MOLECULE TYPE: protein
US-08-211-202-116
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Patent No. 563641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SHREACE RESIDUE
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-07-942-245-37
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Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
Search completed: April 25, 2006, 06:28:40
Job time : 34.7264 secs
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Sequence (Sequence (Sequence

Sequence 6, A Sequence 6, A Sequence 37, Sequence 44, Sequence 90, Sequence 19, Sequence 18, Sequence 18, Sequence 18, Sequence 58, Sequence 58, Sequence 69, Sequence 69, Sequence 69, Sequence 69, Sequence 69, Sequence 69,

OM protein

Run on:

Sequence:

Searched:

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Sequence 65, Application US/10338552
; Sequence 65, Application US/10338552
; Publication No. US20040131612A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jaffry D.
; APPLICANT: Watkins, Lain P.
; APPLICANT: Wasserot, Alain P.
; APPLICANT: Wasserot, Milliam D.
; TITLE OF INVENTION: TNF-alpha Binding Molecules
; TITLE REFERENCE: AME-06971
; CURRENT PILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 65
; SEQ ID NO 65
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-LIC-318-02/-02

Sequence 55, Application US/10338627

Publication No. US20040131613A1

GENERAL INFORMATION

APPLICANT: Watkins, Jeffry D.

APPLICANT: Watkins, David

APPLICANT: Watkins, David

APPLICANT: Watkins, David

APPLICANT: Huse, William D.

TITLE NETERENCS: AME-07497

CURRENT APPLICATION: TNF-alpha Binding Molecules

FILE REFERENCS: AME-07497

CURRENT APPLICATION NUMBER: US/10/338,627

CURRENT FILING DATE: 2003-01-08

NUMBER OF SEQ ID NOS: 92

SOFTWARE: Patentin version 3.2

SEQ ID NO 65

LENGTH: 25

TYPE: PRT

CORGANISM: Homo sapiens

US-10-338-627-65
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100.0%; Pred. No. 5.3e-10;
tive 0; Mismatches 0;
                    US-10-638-210-37
US-10-638-210-44
US-10-842-011-45
US-10-842-011-45
US-09-910-483-45
US-10-194-975-18
US-10-194-975-18
US-10-194-975-18
US-10-194-975-18
US-10-103-0378-69
US-10-032-0378-78
US-10-029-9888-78
US-10-032-9888-78
US-10-032-9888-78
US-10-032-9888-78
US-10-032-9888-78
US-10-032-9888-78
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ORGANISM: Homo sapiens
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Matches 25; C
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US-10-338-627-65
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TYPE: PRT
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Sequence 311, App
Sequence 339, App
Sequence 348, App
Sequence 363, App
Sequence 366, App
Sequence 80, Appl
Sequence 80, Appl
Sequence 4, Appli
Sequence 4, Appli
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121, App
121, App
5, Appli
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28530, A
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Sequence 65, Appl
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Sequence 240,
Sequence 106,
Sequence 39, A
Sequence 28530
                                                                                               April 25, 2006, 06:58:17 ; Search time 108.962 Seconds (without alignments) 95.866 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA Main: * /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-764-428-3

US-10-923-068-315

US-10-923-068-348

US-10-923-068-348

US-10-923-068-348

US-10-923-068-343

US-10-923-068-372

US-10-923-068-372

US-10-915-490-4

US-10-915-490-4

US-09-855-271-17

US-09-855-271-17

US-09-875-271A-121

US-10-923-068-183

US-10-923-068-189

US-10-923-068-207

US-10-923-068-216

US-10-923-068-210
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                                                                                                                                                                                                                                                        1867569 seqs, 417829326 residues
                                                                                                                                                        US-10-764-428-3
123
1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Length 25; Indels

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RESULT 6
US-10-923-068-339
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                                                                                                                                                                                                                               Sequence 3, Application US/10764428
Publication No. US20040229310A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
TITLE OF INVENTION: TIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
TITLE OF INVENTION: CULTURE
FILE REFERENCE: 11669.120USU1
CURRENT APPLICATION NUMBER: US/10/764,428
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/442,484
PRIOR FILING DATE: 2003-01-23
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  Length 25;
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100.0%; Score 123; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0;
ch 100.0%; Score 123; DB 4;
1 Similarity 100.0%; Pred. No. 5.3e-10;
25; Conservative 0; Mismatches 0;
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US-10-923-068-315
; Sequence 315, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AE600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 315
                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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SOFWARE: Patentin version 3.1
SEQ ID NO
LENGTH: 25
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Matches 25; Conservative
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ORGANISM: Homo sapiens
  Query Match
Best Local Similarity
Matches 25; Conserva
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RESULT 5

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Publication No. US20050042664A1

GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Damschroder, Melissa
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
FILE REPERFORCE: ASEGOUS
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT PILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 348
LENGTH: 25
Sequence 321, Application US/10923068
Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: W. Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Dall'Acqua, William
APPLICANT: Dall'Acqua, William
APPLICANT: DamsChroder, Melissa
ITILE OF INVENTION: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AE600US
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 321
LENGTH: 25
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Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: Wu, Herren:
APPLICANT: Damchroder, Melisam
APPLICANT: Damchroder, Melisam
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SEQ ID NOS: 518
SEQ ID NO 339
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-923-068-321
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COGGANISM: Homo sapiens
US-10-923-068-339
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RESULT 11
US-10-751-826-80
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US-10-915-490-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
                                                                        Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 123; DB 5; Length 2
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                             Indels
                                                    100.0%; Score 123; DB 5; dlarity 100.0%; Pred. No. 5.3e-10; Conservative 0; Mismatche.
                                                                                                                                                                                                                                                                           Sequence 363, Application US/10923068

Publication No. US20050042664A1

GENERAL INFORMATION:
APPLICANT: Wi, Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Damschroder, Melissa
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AE6004068;
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT PILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 363
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 366, Application US/10923068
Publication No. US200500426641
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Damschroder, William
APPLICANT: Damschroder, Melissa
TITIE OF INVENTION: HUMANIZATION OF ANTIBODIES
TITIE OF INVENTION: HUMANIZATION OF ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT PILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 366
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-923-068-366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-10-923-068-363
      ; TIFE: FAI
; ORGANISM: Homo sapiens
US-10-923-068-348
                                                                        Query Match
Best Local Similarity
Matches 25; Conserv
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US-10-923-068-363
TYPE: PRT
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RESULT 10 US-10-923-068-372

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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APPLICANT: CASTERMAN, CECTIE
APPLICANT: CASTERMAN, CECTIE
APPLICANT: HAMERS, RAYMOND
TITLE OF INVENTION: INMUNOCLOBULINS DEVOID OF LIGHT CHAINS
FILE REPERENCE: 0.958.0008-07000
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/293,769A
PRIOR PILING DATE: 1999-04-19
PRIOR PILING DATE: 1999-04-19
PRIOR PILING DATE: 1995-06-06
PRIOR PILING DATE: 1995-06-05
PRIOR PILING DATE: 1995-08-21
PRIOR PILING DATE: 1995-08-21
PRIOR PILING DATE: 1993-05-16
PRIOR PILING DATE: 1993-05-11
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100.0%; Score 123; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.5e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 123; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0;
Sequence 372, Application US/10923068
Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: William
APPLICANT: Dail'Acqua, William
APPLICANT: Dail'Acqua, William
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AE600US
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: PateSEQ for Windows Version 4.0
SEQ ID NO 372
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10915490
Publication No. US20050130266Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-10-923-068-372
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APPLICANT: Athwal, Diljeet Singh
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Brown, Derek Thomas
APPLICANT: Chapman, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0089
CURRENT APPLICATION NUMBER: US/09/875,221A
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
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                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                        FEATURE:
CTHER INFORMATION: Consensus
US-09-855-271-17
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Best Local Similarity
Matches 25; Conserva
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LENGTH: 30
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                                                                                          Cornelis T. VERRIPS
TITLE OF INVENTION: Production of antibodies or (functionalized)
fragments thereof derived from heavy chain immunoglobulins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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| Sequence 17, Application US/09855271
| Patent No. US20020042089A1
| GENERAL INFORMATION:
| APPLICANT: Briman. Mark W
| APPLICANT: Briman. Diljeet Singh
| APPLICANT: Emtage, John Spencer
| TITLE OF INVENTION: Interleukin.5 Specific Recombinant Antibodies
| FILE REFERENCE: CARP-0088
| CURRENT PILING DATE: 2001-05-15
| PRIOR APPLICATION NUMBER: 09/347,061
| WUMBER OF SEQ ID NOS: 28
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: human heavy chain framework (subgroup III) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                               ADDRESSEE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: D.C.
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: 1BM FC compatible

CORRUTER: 1BM FC COMPATIBLE

SOFTWARE: MICROSOFT WAS

SOFTWARE: MICROSOFT WAS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/915,490

FILING DATE: 11-Aug-2004

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/537,871

FILING DATE: 28-APR-1996

APPLICATION NUMBER: FC7/EP94/01442

FILING DATE: 28-APR-1994

APPLICATION NUMBER: EPO 9320179.5

FILING DATE: 15-JUL-1993

APPLICATION NUMBER: EPO 93201239.6

FILING DATE: 19-MAY-1993

APPLICATION NUMBER: EPO 93201239.6

FILING DATE: 29-APR-1993
                       Cecile HAMERS-CASETERMAN
Serge V. M. MUYLDERMANS
Leon G. J. FRENKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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                                                                                                                                                                          of Camelidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 26 amino acids
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TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
APPLICANT: Raymond HAMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                              NUMBER OF SEQUENCES: 7. CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Best Local Similarity 100.
Matches 25; Conservative
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US-09-855-271-17
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Query Match 100.0%; Score 123; DB 3; Length 30; Best Local Similarity 100.0%; Pred. No. 6.4e-10; Matches 25; Conservative 0; Mismatches 0; Indels
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US-09-949-559-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 100.0%; Score 123; DB 3;
Conservative 0; Mismatch.
                                                                                                                                                                                                                                                       JOS-09-19-10-121, Application US/09949559

PRECENT NO. US20020151682A1

GENERAL INFORMATION:

APPLICANT: Arhwal, Dilject Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
ITILE REPERENCE: Garp-0095
FILE REPERENCE: Garp-0095
CURRENT APPLICATION NUMBER: US/09/949,559
CURRENT PLING DATE: 2001-12-20
PRIOR PLING DATE: 2001-06-06
PRIOR PLING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
NUMBER: OF SEQ ID NOS: 130
SEQ ID NO 121
SEQ ID NO 121
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April 25, 2006, 07:01:21; Search time 16.0377 Seconds (without alignments) 68.593 Million cell updates/sec
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1. /SIDS5/ptodata/1/pubpaa/USO8 NEW FUB.pep:*
2. /SIDS5/ptodata/1/pubpaa/USO6 NEW FUB.pep:*
3. /SIDS5/ptodata/1/pubpaa/USO7 NEW FUB.pep:*
4. /SIDS5/ptodata/1/pubpaa/PCT_NEW FUB.pep:*
5. /SIDS5/ptodata/1/pubpaa/USO9 NEW FUB.pep:*
7. /SIDS5/ptodata/1/pubpaa/US10_NEW FUB.pep:*
7. /SIDS5/ptodata/1/pubpaa/US10_NEW FUB.pep:*
8. /SIDS5/ptodata/1/pubpaa/US11_NEW FUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                              US-10-764-428-3
123
1 EVQLVRSGGGLVQPGGSLRLSCAAS 25
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                             OM protein
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                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		App	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl										
	g	113,	39,	46,	18,	31,	28,	17,	34,	, 38,	15,	78,	30,	33,	30,	36,	39,	44,	47,	14,	19,	27,	30,	33,	37,	30,
	tio		çe	če	çe	çe	ce	če	ce	ce	če	ice	ce	ဥ	ဥ	See.	ce	ce	og.	ЗĞе	ice	Sc.	JCe	oc.	ice	ce
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	Des	Se	Se	Se	Se	S	Se	S	S	Se	Se	Se	Se	Se	Se	Se	တိ	Š	Se	S	Se	Se	Se	Se	S	Se
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ALIGNMENTS

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DEPLICANT: LAZAR, GREGOTY ALAN
APPLICANT: LAZAR, GREGOTY ALAN
APPLICANT: LAZAR, GREGOTY ALAN
APPLICANT: Desjarlais, John R.
APPLICANT: Hammond, Phillip W.
TITLE OF INVENTION: METHODS OF GREERATING VARIANT PROTEINS WITH INCREASED HOST STRING
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
FILE REFERENCE: 185832/US/5
CURRENT APPLICATION NUMBER: US 60/527,167
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR FILING DATE: 2004-06-21
PRIOR FILING DATE: 2004-06-21
PRIOR FILING DATE: 2004-06-11
PRIOR FILING DATE: 2004-06-13
PRIOR FILING DATE: 2004-06-13
PRIOR FILING DATE: 2004-10-14
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Publication No. US20060024296A1
GENERAL INFORMATION:
APPLICATION THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
FILE REPREBENCE: file
CURRENT APPLICATION NUMBER: US/10/982,357
CURRENT FILING DATE: 2004-11-05
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Best Local Similarity 100.0%; Pred. No. 4.8e-10;
Matches 25; Conservative 0; Mismatches 0;
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Sequence 113, Application US/11004590 Publication No. US20060008883A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                                                                                                   Length 44;
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APPLICANT: PROTein Design Labs
TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
FILE REPRENCE: file
CURRENT APPLICATION NUMBER: US/10/982,357
CURRENT APPLICATION NUMBER: 204-11-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                 Query Match 100.0%; Score 123; DB 6; Best Local Similarity 100.0%; Pred. No. 6.8e-10; Matches 25; Conservative 0; Mismatches 0;
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FILE REFERENCE: 30219/US/3
GURRENT FILING DATE: 2005-02-08
FRIOR APPLICATION NUMBER: US 10/194,975
FRIOR APPLICATION NUMBER: US 60/305,111
FRIOR APPLICATION NUMBER: US 60/305,111
FRIOR PRING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SEQ ID NO 18
LENGTH: 97
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                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 46, Application US/10982357; Publication No. US20060024296A1
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.2
SEQ ID NO 39
LENGTH: 44
                                                                              TYPE: PRT; ORGANISM: Homo sapiens
US-10-982-357-39
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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bublication No. US20050260679A1;
chibication No. USCONTION: Strid-Ai;
chibicant: Koren, Wouter THE RISK OF HUMAN ANTI-HUMAN;
current Application NUMBER: 100/11/084,554
current Application NUMBER: 06/554,372
prior PILING DATE: 2004-03-19;
prior PILING DATE: 2004-03-19;
prior PILING DATE: 2004-03-19;
prior PILING DATE: 2004-05-24;
submare OF SEQ ID NOS: 266
copymare: Paster of Windows Version 4.0
copymare: Paster of Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0;
                                                                       TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/UG3,
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT PILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PATCHIN VERSION 3.3
SEQ ID NO 31
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Sequence 31, Application US/11054669 Publication No. US20050261480Al GENERAL INFORMATION:
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US-11-054-669-31
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US-11-084-554-28
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                                                                              GREAL INCORATION:
GREAT INCORATION:
APPLICANT: Green, Larry L.
APPLICANT: Green, Larry L.
APPLICANT: Green, Larry L.
APPLICANT: Green, Larry L.
TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
FILE OF INVENTION NUMBER: 11/084,554
PRIOR PELICATION NUMBER: 11/084,554
PRIOR PELING DATE: 2005-03-17
PRIOR PELING DATE: 2005-03-17
PRIOR PELING DATE: 2004-03-19
PRIOR PELING DATE: 2004-03-19
PRIOR PELING DATE: 2004-03-19
PRIOR PELING DATE: 2004-03-19
NUMBER OF SEQ ID NOS: 266
SOFTWARE: PARSER (FOR Windows Version 4.0)
SEQ ID NOS: 266
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11 Similarity 100.0%; Pred. No. 1.4e-09;
25; Conservative 0; Mismatches 0;
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100.0%; Score 123; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REPERENCE: 30219/US,
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin Version 3.3
SEQ ID NO 15
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; Publication No. US20050261480A1
; GENERAL INFORMATION:
     Publication No. US20060021074A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Homo sapiens
US-11-136-250-28
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CORGANISM: Homo sapiens
US-11-054-669-15
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Matches 25; Conserv
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| Bequence 34 Application US/11004590
| Publication No. US20060008883A1
| GENERAL INFORMATION:
| APPLICANT: Lazar, Gregory Alan
| APPLICANT: Lazar, Gregory Alan
| APPLICANT: Hammond, Phillip W. |
| TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF |
| TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF |
| TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF |
| TITLE OF INVENTION WUMBER: US 60/527,167 |
| PRIOR APPLICATION NUMBER: US 60/527,167 |
| PRIOR PILING DATE: 2004-06-21 |
| PRIOR PILING DATE: 2004-06-21 |
| PRIOR PILING DATE: 2004-06-21 |
| PRIOR PILING DATE: 2004-10-14 |
| NUMBER OF SEQ ID NOS: 458 |
| SOFTWARE: Patentin version 3.3 |
| SEQ ID NO 34 |
| LENGTH: 97 |
| LE
APPLICANT: Desjarlais, John R.
APPLICANT: Hammond, Phillip W.
TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
CURRENT APPLICATION NUMBER: US 60/527,167
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR PILING DATE: 2004-06-21
PRIOR PILING DATE: 2004-06-21
PRIOR PILING DATE: 2004-06-21
PRIOR PILING DATE: 2004-10-14
NUMBER OF SEQ ID NOS: 458
SEQ ID NOS: 458
SEQ ID NO 17
LENGTH: 97
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100.0%; Score 123; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels
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100.0%; Score 123; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0;
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; Sequence 28, Application US/11136250
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US-11-004-590-34
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US-11-004-590-17
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US-11-084-554-30

| Sequence 30, Application US/11084554
| Publication NO. US2005026679A1
| GENERAL INFORMATION:
| APPLICANT: Kellermann, Sirid-Ai
| APPLICANT: Green, Larry L. APPLICANT: Korver, Wouter
| TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION CURRENT FILING DATE: 2005-03-17
| CURRENT FILING DATE: 2005-03-17
| PRIOR FILING DATE: 2004-03-17
| PRIOR FILING DATE: 2004-03-17
| PRIOR FILING DATE: 2004-03-17
| PRIOR FILING DATE: 2004-05-24
| NUMBER OF SEGIEN OF SEGIEN WINDOWS: SOFTWARRE: FESTERE ONS: 266
| SOFTWARE: FESTERE OF WINDOWS: 266
| SOFTWARE: FESTERE OF WINDOWS: 266
| SOFTWARE: FESTERE OF WINDOWS: 266
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APPLICANT: Korver, Wouter
TITLE OF INVENTION: REDICING THE RISK OF HUMAN ANTI-HUMAN
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
CURRENT APPLICATION NUMBER: US/11/084,554
CURRENT FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: 60/554,372
PRIOR APPLICATION NUMBER: 60/554,661
PRIOR APPLICATION NUMBER: 60/574,661
PRIOR APPLICATION NUMBER: 60/574,661
PRIOR APPLICATION NUMBER: 60/574,661
PRIOR FILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 266
SEQ ID NO 36
LENGTH: 98
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100.0%; Score 123; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0: Indela
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                                                                                                                   100.0%; Score 123; DB 7; ilarity 100.0%; Pred. No. 1.4e-09; Conservative 0; Midmatalar
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                                              ; ORGANISM: Homo sapiens
US-11-054-669-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-30
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100.0%; Score 123; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCORMATION:
GENERAL INFORMATION:
FILE REFERENCE:
GENERAL INFORMATION:
GENERAL INFORM
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Fublication No. US20050261480A1

GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
FILE REFERENCE: 30219/US/3

FURRENT PELLING DATE: 2005-02-08

PRIOR APPLICATION NUMBER: US/11/054,669

CURRENT FILING DATE: 2002-07-12

PRIOR APPLICATION NUMBER: US 60/305,111

PRIOR APPLICATION NUMBER: US 60/305,111

PRIOR APPLICATION NUMBER: US 60/305,111

PRIOR PILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 124

SOFTWARE: PRECEIT VERSION 3.3

LENGTH: 98
FILE REFERENCE: 30219/US/3
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT PILING DATE: 2005-02-08
FRIOR APPLICATION NUMBER: US 10/194,975
PRIOR FILING DATE: 2002-07-12
PRIOR PILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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US-11-054-669-30
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ö Gaps °; Best Local Similarity 100.0%; Pred. No. 1.4e-09; Matches 25; Conservative 0; Mismatches 0; Indels

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Search completed: April 25, 2006, 07:10:01 Job time : 16.2044 secs

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- protein search, using sw model OM protein

Run on:

April 25, 2006, 06:15:41; Search time 8.49057 Seconds (without alignments) 113.322 Million cell updates/sec

US-10-764-428-14 58

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 GYTFTNYGIN 10 Title: Perfect score: Scoring table: Sequence:

283416 segs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

PIR 80: *
1: pirl: *
2: pir2: *
3: pir3: *
4: pir4: * **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	. ! .	heavy		heavy	heavy chain	heavy chain	mAb heavy ch	heavy chain	heavy chain	heavy chain	heavy chain V	heavy	heavy	heavy	heavy	heavy	heavy chain V	heavy chain V	heavy chain V	heavy chain V	heavy	heavy	heavy cha	Ig heavy chain V r						
QI		A36194	C24672	S26326	D24672	S24764	824765	S26325	819968	S19965	S19967	A53285	B42848	PH1404	833905	B28572	B24754	A28572	PH1491	PH1490	PH1523	PH1522	838565	A24754	PH1510	PH1505	PH1518	PH1517	PH1502	PH1500
Lenath DB					101 2				115 2						46 4				102 2	102 2	114 2				119 2		119 2			119 2
* Query Match Lend		100.0	æ.	₩.		۵.	8.8	4.8	4.8	4.8	4.8	۳.	4.8	80.	8	4.	4.	4.	4	4.	4.	4.	1.4	1.4	4.	4.	1.4	4.	4.	91.4
Score		28	52	55	55	55	55	55	55	55	55	55	55	55	55	23	53	53	53	53	53	53	53	23	53	53	53	53	53	23
Result		-	7	e	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	70	21	22	23	24	25	26	27	28	29

Ig heavy chain V r	
PH1503 PH1504 PH1520 A24854 A24854 A24854 PH1492 PH1492 PH1483 PH1483 PH1482 PH482 P	9860Hd
000000000000000000	4 (4
1119 1119 1121 1135 1140 1140 1170 1170 1170 1170	111
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	89.7 87.9
	275
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 5 5

ALIGNMENTS

RESULT 1

Is belly that I vegion (clone 284.1) - mouse (c) Species: Mus musculus (house mouse) (c) Species: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 16-Aug-1996 (c) Spacession: A36194 (c) Spacession: A36194 (c) Spacession: A37-548, 1990 (c) A; Reference number: A36194; MUID:91029486; PMID:2121365 (c) A; Reference number: A36194 (c) MUID:91029486; PMID:2121365 (c) A; Residues: DNA A; Residues: DNA A; Residues: UNA A; Residues: UNA A; Residues: UNIPARC:UPI0000176C50; GB:M38389 (c) Superfamily: immunoglobulin V region; immunoglobulin homology (c) Keywords: heteroterramer; immunoglobulin homology < IMM>

Gape ö Query Match
100.0%; Score 58; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 10; Conservative 0; Mismatches 0; Indels

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RESULT 2

Grace was chain V region (VMU-1) - mouse (fragment)
Crispecies: Mus musculus (house mouse)
Crispecies: Mus musculus (house mouse)
Crispecies: Mus musculus (house mouse)
Crispecies: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
Crispecies: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
Crispecies: 1-2867, 1985
Archive and Archive and

Gaps ö Query Match

94.8%; Score 55; DB 2; Length 93;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels

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1 GYTFTNYGIN 10

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A;Molecule type: DNA
A;Residues: 1-105 <THO>
A;Cross-references: UNIPARC:UPI000011648C; EMBL:Z15020; NID:g52616; PIDN:CAA78739.1; PID
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Accession: S26325
R,Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-64, 1991
A,Title: Antibodies that are specific for a single amino acid interchange in a protein eg A,Title: Antibodies that are specific for a single amino acid interchange in a protein eg A,Title: Antibodies that are specific for a single amino acid interchange in a protein eg A,Reference number: S26309, MUID:91341421; PMID:1908510
A,Rocession: S26325
A,Status: preliminary
A,Rolecule type: mRNA
A,Rolecule type: mRNA
A,Residues: 1-109 <STA>
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C;Species: Wus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence revision 21-Nov-1998 #text_change 23-Jul-1999
C;Accession: S24765; S24773; S24778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 105;
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A;Molccule type: DNA
A;Residens: 1-105 «KLA»
A;Residenses: UNIPARC:UPI000011648E; EMBL:Z15001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPARC: UPI000011648B; EMBL: 215013
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Pred. No. 0.013;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                           94.8%; Score 55; DB 2;
90.0%; Pred. No. 0.013;
tive 1; Mismatches
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submitted to the EMBL Data Library, August 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Thomas, J.W.
submitted to the EMBL Data Library, August 1992
A;Reference number: S24776
AAccession: S24778
submitted to the EMBL Data Library, August 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 94.8%;
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 90.0
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                                   A;Reference number: S24776
A;Accession: S24777
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A; Residues: 1-105 < KLW>
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A; Residues: 1-105 <THO>
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Best Local S
Matches 9
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A;Redidues: 1-101 ANIN>
A;Cross-references: UNIPARC:UP10000113758; GB:X03301; NID:g51757; PIDN:CAA27040.1; PID:gA;Cross-references: UNIPARC:UP10000113758; GB:X0505: Libis sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C;Date: 18-623.6
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: S26309; MUID:91341421; PMID:1908510
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19 heavy chain V region (VGAM3-8) - mouse (fragment)

C;Species: Miss musculus (house mouse)

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C;Accession: D24672

R;Minter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A;Reference number: A91022; MUID:86055722; PMID:2998759
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Gradue: 20-Peb-1995 #sequence revision 21-Nov-1998 #text_change 23-Jul-1999
Rradue: 324764
Arrestore number: 524763
Arrestore number: 524764
Arrestore number: 524763
Arrestore number: 524764
Arrestore number: 524764
Arrestore number: 524764
Arrestore number: 524772
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A;Residues: 1-99 <STA>
A;Croselsereferences: UNIPARC:UPI00001769AC; EMBL:X59174
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.8%; Score 55; DB 2; Length 101; 90.0%; Pred. No. 0.012; tive 1; Mismatches 0; Indels
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A;Cross-references: UNIPARC:UPI000011648C; EMBL:Z15011
R;Thomas, J.W.
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Pred. No. 0.012;
1; Mismatches
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90.0%;
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Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Query Match

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Tue Apr 25 08:25:42 2006

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19.96ayy chain V region (M-T321) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06.Peb-1995 #sequence_revision 06.Peb-1995 #text_change 31-Dec-2004
C;Accession: 819965
R;Weissenhorn, W.; Riethmueller, G.; Weiss, R.M.; Rieber, B.P.
R;Weissenhorn, W.; Riethmueller, G.; Weiss, R.M.; Rieber, B.P.
A;Description: Structural characterization of CD4 mAb.
A;Reference number: 819963
A;Stetus: prediminary
A;Accession: 819965
A;Stetus: prediminary
A;Molecule type: mRNA
A;Residues: 1-115 <WRI>A;Residues: 1-115 <WRI>A;Cross-references: UNIPROT: 0921A6; UNIPARC: UPI0000176968; EMBL: X65088
C;Ruperfamily: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 31-Dec-2004
C;Accession: S1996s
B;Weissenhorn, W.; Riethmueller, G.; Weiss, B.M.; Rieber, B.P.
B;Weissenhorn, W.; Riethmueller, G.; Weiss, B.M.; Rieber, B.P.
A;Poscription: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Accession: S19568
A;Accession: S19568
A;Status: preliminary
A;Molecule type: mRNAA
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A;Cross-references: UNIPROT:Q921A6; UNIPARC:UP1000017696A; EMBL:X65089
C;Superfamily: immunoglobulin homology
C;Roywords: heterotetramer; immunoglobulin
F;10-93/Domain: immunoglobulin homology <IMM>
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                                                                                       Score 55; DB 2; Length 109;
Pred. No. 0.013;
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Ig heavy chain V region (M-T406) - mouse (fragment)
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11arity 90.0%; Pred. No. 0.014; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                     1; Mismatches
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;S-88/Domain: immunoglobulin homology <IMM>
                                                                                            94.8%;
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                                                                                                               Local Similarity 90.0
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Matches 9; Conserv
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hes 9; Conserv
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E.Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 103-1072, 1991
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary strucand their pH-reactivity profiles.
A;Reference number: A53285; MUID:92017897; PMID:1922102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA; protein
A; Molecule type: DNA; protein
A; Mesidues: 1-19 eSAM-
A; Cross-references: UNIPARC: UDIO00011D0A7; GB: D12736; NID: g220595; PIDN: BAA02228.1; PID: A; Cross-references: UNIPARC: UDIO00011D0A7; GB: D12736; NCBIN: 63271, NCBIN: 63299)
A; Note: sequence extracted from NCBI backbone (NCBIN: 63271, NCBIP: 63299)
C; Superfamily: immunoglobulin vegion; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Date: 27-Apr-1993 #sequence_revision, D; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffc
R;Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffc
J. Biol. Chimeric L6 anti-tumor antibody. Genomic construction, expression, and characte
A;Reference number: A42848; MUID:92348410; PMID:1639794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-120 «PEL»
A;Cross-references: UNIPARC:UP10000115333; GB:M90690; NID:g195065; PIDN:AAA38146.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBIP:109961)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V and J regions, monoclonal antibody SCET.M8.1 - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 31-Dec-2004
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                                     C;Accession: S19967
R;Weissenhorn, W.; Rtethmueller, G.; Weiss, E.M.; Rieber, E.P.
R;Weissenhorn, W.; Rtethmueller, G.; Weiss, E.M.; Rieber, E.P.
R;Weissenhorn, W.; Rtethmueller, G.; Warch 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Reference number: S19963
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 < WEI>
A;Cross-references: UNIPROT:Q921A6; UNIPARC:UPIO000176969; EMBL:X65090
A;Cross-references: UNIPROT:Q921A6; UNIPARC:UPIO000176969; EMBL:X65090
C;Superfamily: immunoglobulin homology
C;Reywords: heterotetramer: immunoglobulin
F;12-95/Domain: immunoglobulin homology < IMM>
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Pred. No. 0.014;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.8%; Score 55; DB 2;
90.0%; Pred. No. 0.014;
iive 1; Mismatches
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Best Local Similarity
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Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)

Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)

Is blackeds: Mus musculus (house mouse)

C; Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000

C; Accession: PH1404; PH1406

R; Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta J. Exp. Med. 176, 1209-1214, 1992

J; Exp. Med. 176, 1209-1214, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
333905
Ig heavy chain precursor V region - synthetic
G;Species: synthetic
C;Species: synthetic
C;Date: 13-Jan-1995 #sequence_revision 30-Apr-1998 #text_change 20-Oct-2000
C;Date: 13-Jan-1995 #sequence_revision 30-Apr-1998 #text_change 20-Oct-2000
B;Jaceselan: 339905
B;July, A.Y.; Robinson, R.R.; Hellstroem, K.E.; Murray Jr., E.D.; Chang, C.P.; Hellstroem Proc. Natl. Acad. Sci. U.S.A. 84, 3439-3443, 1987
A;Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells.
A;Reference number: S33905; MUID:87204152; PMID:3106970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: S33905
Modecule type: mRNA
A,Residues: 1-146 c.11U5
A,Cross-references: UNIPARC:UPI0000114C7D; EMBL:M16072; NID:g195270; PIDN:AAA38229.1; PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.8%; Score 55; DB 2; Length 124; illarity 90.0%; Pred. No. 0.015; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 4; Length 146;
Pred. No. 0.018;
1; Mismatches 0; Indels
A,Cross-references: UNIPARC:UPI0000115333; EMBL:M90691
C,Superfamily: immunoglobulin V region; immunoglobulin homology
F,15-98/Domain: immunoglobulin homology <IMM>
                                                                                             Length 120;
                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: PH1403; MUID: 93018837; PMID: 1402663
                                                                                                Score 55; DB 2;
Pred. No. 0.014;
                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPARC:UP1000017694C
A,Accession: PH1406
A,Molecule type: DNA
A,Residues: 115-121
A,Cross-references: UNIPARC:UP1000017694C
                                                                                                  94.8%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Matches 9; Conservative
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Matches 9; Conserv
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A; Residues: 1-124 <SHI>
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RESULT 15

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A;Molecule type: DNA
A;Residues: 1-76 cSIE>
A;Cross-references: UNIPARC:UPI0000114908; GB:K02154; GB:M17032; NID:g196176; PIDN:AAA380
A;Cross-references: UNIPARC:UPI0000114908; GB:K02154; GB:M17032; NID:g196176; PIDN:AAA380
A;Note: Limences was determined from the germline gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
Igheavy chain V regions (CR-Id 7, CR-Id 14) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jul-2000
C;Accession: B26572
R;Siekevitz, M.; Huang, S.Y.; Gefter, M.L.
R;Siekevitz, M.; Huang, S.Y.; Gefter, M.L.
Bur. J. Immunol. 13, 123-132, 1983
A;Title: The generic basis of antibody production: a single heavy chain variable region A;Reference number: A91262; MUID:83157801; PMID:6403356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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91.4%; Score 53; DB 2; Length 76;
Best Local Similarity 90.0%; Pred. No. 0.021;
Matches 9; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: April 25, 2006, 06:26:11
Job time : 9.49057 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 GYTFTSYGIN 20
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OM protein - protein search, using sw model

April 25, 2006, 06:05:44 ; Search time 53.3962 Seconds (without alignments) 132.131 Million cell updates/sec Run on:

US-10-764-428-14 58 1 GYTFTNYGIN 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		,			SUMMARIES	
Result	9705	Query	Length	ä	1	Description
	2					
1	53	91.4	120	7	HV03 MOUSE	EUE
7	53	91.4		-	HV02_MOUSE	EUM
e	20	86.2		~	Q921A6 MOUSE	_
4	20	86.2		~	QSPQS1_RAT	
ហ	47	81.0		~	QSHZY6 MOUSE	6
9	46	79.3		Н	HV52_MOUSE	_
7	46	79.3		N	OSBJZ2_RAT	
80	46	79.3	463	N	Q99LC4_MOUSE	-
6	45	77.6		~	O6PILO HUMAN	Qépilo homo sapien
10	45	77.6		~	Q65ZL3_9MURI	_
11	45	77.6	233	~	Q4ZGV0 9BACT	0 unid
12	44	75.9		٦	HV01 MOUSE	mus
13	44	75.9		~	Q569W9 MOUSE	mus (
14	44	75.9		7	Q9D8L4_MOUSE	mus
15	44	75.9		N	Q4V9V8_MOUSE	
16	43	74.1		7	Q6X2N8_9BACT	
17	43	74.1		7	Q6X2P6_9BACT	
18	43	74.1		~	Q6X2P9_9BACT	
19	43	74.1		~	Q8RT26_9BACT	
20	43	74.1	220	~	Q9AP60_9BACT	-
21	43	74.1			Q9AP61_9BACT	-
22	43	74.1		N	Q9AP62_9BACT	-
23	43	74.1	220		Q9AP63_9BACT	
24	43	74.1			Q6X2Q0_9BACT	
25	43	74.1			Q6X2P0_9BACT	-
56	43	74.1			Q6X2N9_9BACT	-
27	43	74.1			Q4ZGQ6_9BACT	_
28	43	74.1	233		Q4ZGQ7_9BACT	unidentifi
59	43	74.1			Q4ZGR1_9BACT	unidentifi
30	43	74.1			Q4ZGR9_9BACT	unidentifi
31	43	74.1	233		Q4ZGSO_9BACT	Q4zgs0 unidentifie

Q4zgs4 unidentifie Q4zgt7 unidentifie Q4zgt7 unidentifie Q5zg43 unidentifie Q5cj4 cryptospori D1771 homo sapien Q5Gg80 homo sapien Q5Gg80 homo sapien Q5CZP4 uncultured Q6xzp4 uncultured Q6xyy uncultured Q6xyy uncultured Q5d3g1 uncultured Q5d3g1 uncultured Q5d3g1 uncultured Q5d3g4 uncultured
04ZGS4_9BACT 04ZGT7_9BACT 04ZGT7_9BACT 04ZGT3_9BACT 05CJA1_CRYHO 05CJA1_CRYHO 05CJA1_CRYHO 05CZG0 HUMAN 06KZQP4_9BACT 06KZQP4_9BACT 06KZQP4_9BACT 06KZQP4_9BACT 05CJG1_9BACT 05CJG1_9BACT
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ALIGNMENTS

MOUSE STANDARD; PRT; 120 AA. HV03_MOUSE STANDARD; PRT; 120 AA. 21-JUL-1986 (Rel. 01, Carted) 21-JUL-1986 (Rel. 01, Last sequence update) 11-SRP-2005 (Rel. 48, Last annotation update) 19 heavy chain v region 36-65.	Mus musculus (Mouse). Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukarmalia; Butheria; Chordata; Craniata; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. NCBI_TAXID=10090; [1] NUCLECTIDE SEQUENCE. NUCLECTIDE SEQUENCE. Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,	Marchak-Rothstein A.; "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse."; Eur. J. Immunol. 12:1023-1032(1982). [2] KARY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-120. MEDLINE-21528949; PubMed=11673524; Parhami-Seren B., Viswanathan M., Strong R.K., Margolies M.N.; Parhami-Seren B., Viswanathan M., Strong R.K., and low-affinity p-	Azophenylargonate-specific antibodies generated by alanine scanning of heavy chain complementarity-determining region 2."; J. Immunol. 167:5129-5135(2001). -1. MISCELLANBOUS: From analysis of the sizes of several other differentiated genes that hybridize to this one, the authors conclude that all of these V regions have rearranged to the same J segment, JH2. -1. SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	PDR; A94264; HVMSG7. PDB; 1JFO; X-ray; H=1-120. Ensembl; ENSWUSG0000021155; Mus musculus. EnterPro; IPR00110; Ig-11ke. InterPro; IPR003596; Ig_v. SWART; SWO6406; IGV; 1. 3D-structure; Hybridoma; Immunoglobulin domain; Immunoglobulin V region. DOMAIN 1 111 DOMAIN SEQÜENCE 120 AA; 13307 WW; FF04E4A167B654AF CRC64;
ST 6 (Rel. 6 (Rel. 5 (Rel. hain V	us (Mou Metazo Eutheri Muridae)=10090; SEQUEN 131846; M., Ge£	thstein ic basi response munol. TALLOGR 528949; iren B.,	ir compl. i. 167:51 i. 167:51 i.anbous centiate ide that it, JH2.	a-Prot e the Swis	54; HVME; X-ray; X-ray; ENSMUSGC IPR0071 IPR0035 10406; ISSO835; Ixe; Hykur, Ixe; Ixe; Ixe; Ixe; Ixe; Ixe; Ixe; Ixe;
RESULT 1 HV03_MOUSE LD HV03_MOUSE AC P01747; DT 21-UU-1986 DT 31-SEP-2005 DT 13-SEP-2005 DE IG heavy chi	Mus musculus (Mou Bukaryota; Metazo Mammaliatuheri Muroidea; Muridae NCBI_TaxID=10090; [1] NUCLEOTIDE SEQUEN MEDLINE=83131846; Siekevitz M., Gef	Marshak-Ro "The genet idiotype r idiotype r Eur. J. Im [2] X-RAY CRYS MEDLINE=21 Parhami-Se	azophenylare heavy chain J. Immunol. -!- MISCELLE differer conclude segment,	This Swiss between t the Europe use as lon removed.	PIR; A9426 PDB; 1JPQ; Engembl; EnterPro; SMART; SMO RNOSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSIDE; PROSI
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Muridae, Murinae, Mus.
                                NCBI_TaxID=10090;
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QSPQS1_RAT
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                         Gaps
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HSSP; P01747; 1JFQ.
SMR; P01746; 20-140.
InterPro; IPR00310; Ig-like.
InterPro; IPR003596; Ig_v.
SMRT; SM00406; IGV;
PROSITE; PS50815; IG LIKE; 1.
PROSITE; PS50815; IG LIKE; 1.
Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin heavy chain.";
Science 216:309-311(1982).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.4%; Score 53; DB 1; Length 140; 90.0%; Pred. No. 0.18;
                    DB 1; Length 120;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-CEA 79 single chain Fv (Fragment).
                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
19-JWX-2005 (Rel. 47, Last annotation update)
19 heavy chain V region 9367 precursor.
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                Score 53; DB 1; Pred. No. 0.15;
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                    91.4%;
90.0%;
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Best Local Similarity 90.05,
Sina 9; Conservative
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Q921A6;
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P01746;
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X REDINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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Brownstein M.J., Usdin T.B., Toshhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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EMBL: U88667; AAB48044.1; -; MENA.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinee; Rattus.
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MUCLEOTIDE SEQUENCE.
MEDLINE-99170165; PubMed=9509426;
Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
I.K.S., Suh P.G., Ryu S.H., Chung H.K.;
"Cloning and characterization of CDNAs encoding VH and VL of a
monocolonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
generation of a single-chain FV molecule (SCFV).";
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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PIR; S19965; S19967.
PIR; S19968; S19967.
PIR; S26325; S26325.
HSSP; PO1607; 1BWW.
Engembl; RSWNGSGO000221155; Mus musculus.
InterPro; IPR007110; IG_N.
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PROSITE; PS50835; IG_LIKE; 2.
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QSPQS1;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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A Klauner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards B., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards B., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Rodriguez A.C., Grimwood J., Schewtenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

B. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

B. Beneration and initial analysis of more than 15,000 full-length human M. Mannes Chun.
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      Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodziguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.R., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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InterPro; IRR0013599; IG.
InterPro; IRR003006; Ig-like.
InterPro; IRR003006; Ig-MrC.
InterPro; IRR003596; IG.
InterPro; IRR003596; IG.
SWART; SM00407; IG.3.
SWART; SM00407; IG.1; 3.
SWART; SM00406; IGV; 1.
PROSITE; PSS0835; IG LIKE; 3.
PROSITE; PS0835; IG LIKE; 3.
PROSITE; PS0835; IG LIKE; 3.
SEQUENCE 475 AA; 52118 MW; RC61093E69A96708 CRC64;
                                                                                                                                                                  NIH MGC Project;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC087057; AAH87057.1; -; mENA.
GO; GO:0003823; P:antigen binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSHZY6_MOUSE PRELIMINARY;
QSHZY6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GYTPTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 GYTPTDYGMN 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOC544903 protein.
Name=LOC544903;
                                                                                                                                                     rissum=Lung;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig heavy chain V region VH558 Al/A4 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;
Yancopoulog G.D., Alt P.W.;
"Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region VH558 Al/A4.
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                                                             Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL, BCO8837; AAH88837.1; -; mRNA.

R GO; GO:0003823; F:antigen binding; IEA.

R InterPro; IPR007110; Ig-11ke.

R InterPro; IPR007599; Ig C1.

R InterPro; IPR003597; Ig C1.

R InterPro; IPR003509; Ig MHC.

R InterPro; IPR003509; Ig MHC.

R InterPro; IPR003509; Ig MHC.

R SMART; SM00409; IG A.

R SMART; SM00409; IG A.

R SMART; SM00409; IG G1.

R PROSITE; PS50835; IG LIKE; 4.

R PROSITE; PS608209; IG MHC; UNKNOWN 2.

R PROSITE; PS608209; IG MHC; UNKNOWN 2.
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Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-2. Pramework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; I.
PROSITE; PS0815; IG LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.0%; Score 47; DB 2;
80.0%; Pred. No. 7.4;
iive 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA.
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BIR; AGO2029; HYWSA1.
PISP, PO1820; 1G7J.
SMR; PO6327; 20-117.
NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Colon;
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Matches 8; Conservative
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49
54
68
85
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                                                       NIH MGC Project;
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Richander R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stepleton M., Soarse M.B., Bonaldon M.F., Carninci P., Frange C.,
Brownstein M.J., Usdin T.B., Toodhyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria, Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I. FUNCTION: Beta-2-microglobulin is the beta-chain of major histocompatibility complex class I molecules (By similarity).
I. SUBCELLULAR LOCATION: Secreted (By similarity).
EMBL; BC091272; AAH91272.1; -; mRNA.
SMR; QSBUZ2; 21-454.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                          Score 46; DB 1; Length 117;
Pred. No. 2.7;
1; Mismatches 1; Indels
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NIH MGC Project;
NIH MG
41 115 By similarity.
117 117
117 AA; 12971 MW; 8BOBC138856DFC9D CRC64;
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SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   458 AA.
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InterPro; IPR003599; IG.
InterPro; IPR003597; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR00409; IG.3.
INTERPRO; IG.3.
INTERPRO; IG.3.
INTERPRO; IG.3.
INTERPRO; IG.3.
INTERPRO; IG.3.
INTERPRO; IG.3.
                                                                                                                                                                   79.3%;
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                                                                                                                                                                                                                                                       Conservative
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Q5bJz2_rat preliminary;
Q5bJz2;
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Best Local Similarity
Local 8; Conserv?
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                                       NON TER
SEQUENCE
DISULPID
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OCSBJ25RA
OCSBJ27RA
OCSBJ2
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A Strengton M. J. Scholler, The Manager M. Scholler D. Monton Old

KY Straughberg Luken by bhopsy.

KY Straughberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KIGUINE-2238827; PubMed-1247732; DOI=10.1073/pnas.242603899;

KA Straughberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KIGUINE-2238827; PubMed-1247732; DOI=10.1073/pnas.242603899;

KIGUINE-2238827; PubMed-1247732; DOI=10.1073/pnas.242603899;

KA Straugher R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Alteschuld S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diafchenko L., Marughan R., Farmer A.A., Rubin G.H., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton R., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaxd G.G.,

Blakesley R.W., Touchman J.W., Gren B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Gren B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rederation and initial analysis of more than 15,000 full-length human
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WCI; WCI:96646; 194-4.

GO; GO:0003823; P:antigon binding; IDA.

GO; GO:001973; P:antibocterial humoral response (sensu Verte. . .; IDA.

GO; GO:001973; P:antibocy-dependent cellular cytotoxicity; IDA.

GO; GO:001978; P:complement activation, classical pathway; IDA.

GO; GO:0042830; P:defense response to pathway; IDA.

GO; GO:006911; P:phagocytosis, engulation iDA.

GO; GO:0006910; P:phagocytosis, recognition; IDA.

GO; GO:005778; P:positive regulation of immune response; IDA.

GO; GO:00576; P:positive regulation of type I hypersensitivity; IDA.

GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.

GO; GO:0001988; P:positive regulation of type I hypersensitivity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=FVB/N;
TISSUB=Mammary_tumor. Metallothionien-TGF alpha model. 10 month old
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Length 458
                                                                         Indels
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Submitted (FRB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -; mRNA.
PIR; B45837; B45837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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       2;
                                                                                                                                                                                                                                                                                                                                                                                                 463 AA.
       Score 46; DB Pred. No. 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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       79.38;
                                        80.08;
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                                                                                                                                                                                                                                                                                                                                                                    Q99LC4 MOUSE
ID Q99LC4 MOUSE PRELIMINARY;
AC Q99LC4;
                                                                         8; Conservative
                                                                                                                                                  1 GYTFTNYGIN 10
                                                                                                                                                                                                                    45 GYTFTNYDIH 54
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SMR; Q99LC4; 21-459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
       Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090
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Pred. No. 4.4;

70.0%;

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Best Local Similarity
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065ZL3 9MURI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Felngold B.A., Grouse L.H., Derge J.G., Altachul S.F., Zeolerge T.E., Shenmen C.M., Schuler G.D., Altachul S.F., Zeolerge T.E., Mark J.E., Mark J.E., Mang J., Haish F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Uddin T.B., Toshiyuti S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A., Gunaratne P.H., Nilalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Antering M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Antering M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Antering M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Antering M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Antering M., Madan A., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.B., Behnerch A., Schein J.B., Whara M.A., Schein J.B., Warra M.A., Schein J.B., Obose S.J.M., Marra M.A., Schein J. Length human M. M. Ganeration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                   79.3%; Score 46; DB 2; Length 463; 70.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                             Indela
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NIH MGC Project;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC03273; AAH32733.1; -; mRNA.
HSSP; P01751; 1A6W.
SWR; Q6PILO; 20-117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 AA; 13913 MW; B76CB434F5A69788 CRC64;
  InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_w.
Pfam; PP07654; C1-8et; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
Immunoglobulin domain.
SEQUENCE 463 AA; 51008 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC, HGNC:5669, IGHV7-81.
InterPro, IPR007110; Ig-like.
InterPro, IPR00356; Ig-v.
SMRAT; SM00406, IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEPILO_HUMAN PRELIMINARY;
QEPILO;
                                                                                                                                                                                                                                                         Query Match 79.3
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sednences.
                                                                                                                                                                                                                                                                                                                                                                      1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                            GYTFTGYGVS 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGHV7-81 protein.
Name=IGHV7-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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OGP 110 HU

OG PILO HU

OG PILO HU

OG PILO HU

OG PILO HO

OG PILO

OG PILO HO

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DB 2; Length 125;

77.6%; Score 45;

Query Match

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MEDLINE=96269537; PubMed=8699031; DOI=10.1016/0022-1759(96)00043-9;

MEDLINE=96269537; PubMed=8699031; DOI=10.1016/0022-1759(96)00043-9;

Nobel D., Bernardi T., Navarro-Teulon I., Martin M., Martinetto J.P.,

And Ducancel F., Mani J.C., Pau B., Piechaczyk M., Biard-Piechaczyk M.;

Analysis of the individual contributions of immunoglobulin heavy and light chains to the binding of antigen using cell transfection and light chains to the binding of antigen using cell transfection and J. Immunol. Methods 193:177-187(1996).

BEBL; S82422; AAB37434.2; -; MRNA.

SMR; G65213; 20-140.

RICEPPC; IPR003599; IG.

RICEPPC; IPR003599; IG.

RICEPPC; IPR003599; IG.

RICEPPC; IPR003599; IG.

RESMART; SM00409; IG.1.

RESMART; SM00406; IG.1.
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dambreville C., Philippot L.,
Structure and activity of the denitrifying community in a maize
"Structure and activity of the denitrifying community in a maize
planted activity of the BMBL/denBank/DBB databases.

EMBL, DQ010807, AAY30755.1; -; Genomic_DNA.

InterPro, IPR001365, Copper_CuA.

InterPro, IPR002429; Cyt_c_ox_2.

Pfam; PF00116; COX2; 1.
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    Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 140 AA; 15302 MW; 7BFE237F3D965F43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.6%; Score 45; DB 2;
77.8%; Pred. No. 4.9;
tive 2; Mismatches
    2; Mismatches
                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nitrous oxide reductase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, environmental samples
                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
Tg10H (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 9BACT
Q4ZGV0_9BACT PRELIMINARY;
                                                                                                                                                                                                     QESZL3 9MURI PRELIMINARY;
QESZL3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.6
Best Local Similarity 77.8
Matches 7; Conservative
      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unidentified bacterium
                                                  2
                                                                                           54
                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Eu
Muridae; Murinae; Mus.
NCBI TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||:||:
GYTFTSYGL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GYTFTNYGI 9
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                                                  1 GYTFTNYGIN
                                                                                           45 GYSPTTYGMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=2338;
                                                                                                                                                                                                                                                                                                                                     Name=Tg10H;
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TISSUE-Mammary tumor metaatatized to lung. Tumor arose spontaneously;

KX TISSUE-Mammary tumor metaatatized to lung. Tumor arose spontaneously;

KX KEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KR Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S. I., Wang J., Haleh F.,

A Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Haleh F.,

B Jatchenco H., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,

RABA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raber J., Heltone E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roderzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CZECH II; TISSUB=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | NIH MGC Project; | NIH MGC Project; | Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases. | Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases. | R MSH; Q56997; 20-464. | NG1; MG1:96443; Igh-la. | R GJ; GG:0003823; F:antigen binding; IEA. | R InterPro; IPR003823; F:antigen binding; IEA. | InterPro; IPR003829; Ig -1ike. | InterPro; IPR003899; Ig -1ike. | R InterPro; IPR004899; IG -1ike. | R InterPro; IPR094899; IG -1ike. | R InterPro; IPR094899; IG -1ike. | R InterPro; IPR09499; IRR09499; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 468 AA; 51666 MW; 5BF6E527329F8461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 2;
Pred. No. 25;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 AA.
                                                         Created)
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80.0%;
                                                      (TrEMBLrel. 30, TrEMBLrel. 30, (TrEMBLrel. 30,
  OS69W9 MOUSE PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
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                                                                                                                                    Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                              WCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CZECH II;
                                                   10-MAY-2005 (
10-MAY-2005 (
10-MAY-2005 (
                                                                                                                                                                         Name=Igh-la;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=81053741; PubMed=6253904; Zakut R., Cohen J., Givol D.; "Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11."; Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8:4839-4840(1980).
--- MISCELLANEOUS: This sequence was translated from an mRNA isolated from a myeloma that secretes 19G2b.
--- SIMILARITY: Contains 1 1g-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                 77.6%; Score 45; DB 2; Length 233; 70.0%; Pred. No. 8.1; 1; Mismatches 2; Indels
                                                                                                             26271 MW; 194F23F11497D008 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ensembl; ENSMUSG0000062635; Mus musculus.
InterPro; IPR007110; 19-1ike.
InterPro; IPR003596; 1g-1.
SWART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region.
DOMAIN 1 112 Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
110-MAY-2005 (Rel. 47, Last annotation update)
Hobary chain V region MPC 11.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
ProDom; PD000131; Copper CuA; 1.
PROSITE; PS50857; COX2 CUA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM, AND SEQUENCE REVISION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.98;
                                                                                                                                             Query Match
Best Local Similarity 70.0°
----- 7; Conservative
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Best Local Similarity 88..
8; Conservative
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190 GYCITNYGVN 199
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HSSP; P01751; 1NQB.
SMR; P01745; 1-121.
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233 AA;
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NUCLEOTIDE SEQUENCE.
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P01745;
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SEQUENCE
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Q569W9_MOUSE
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               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
11brary, clone:1810060009 product:immunoglobulin heavy chain 6 (heavy
chain of IgM), full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/61; TISSUE=Pancreas; MEDLINE=9927953; PubMed=1034636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Medth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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WINTELEOTIDE SEQUENCE.

REDINE_20530913; Pubmed=11076861; DOI=10.1101/gr.152600;

REDINE_20530913; Pubmed=11076861; DOI=10.1101/gr.152600;

Shibate K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Kunamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

Pujiwake S., Inoue K., Togawa Y., Tanawa T., Matsuura E., Watshiki M.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

"RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Pancreas; The FANTOM Consortium,
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                                                                                                                                                                                                                                                                                                              Muridae; Murinae; Mus.
                                                                                                                                                                                                                              Mus musculus (Mouse).
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Q9DBL4;
01-JUN-2001 (
01-JUN-2001 (
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Arakawa T., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiracoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Salto H., Saito H., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Tejima Y., Toya T., Yanamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatuu M., Hayashizaki Y.,
Rabited (UUL-2000) to the EMBL/GenBank/DDBJ databases.
BENBL, AKO07918; BAB25349.1; -; mRNA.
RIR; S19966; S19966.
RIR; S19966; S19966.
RIR; S1879; PO1864; 1BOG.
RIR; OSBEL 1BOG.
RIR; OSBEL 1BOG.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin domain.
SEOUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                            Ensembl; ENSMUSG0000054328; Mus musculus.
MGI; MGI:96443; Igh-la.
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PROSITE; PS00290; IG MHC; UNKNOWN_1.
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                                             NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Pancreas;
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Q4v9v8;
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les 8; Conservative
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NUCLECOTIDE SEQUENCE.

NUCLECOTIDE SEQUENCE.

TISSUE=Mammary gland;

MEDINEE-238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buetow K.H., Schamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhata N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Haiteh F.,

Applation M., Soares M.B., Bonaldo M.F., Gasvant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

Raba S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Warra M.A.,

Butterfield W.S., Jones B.J.M., Marra M.A.,

Butterfield W.S., Worley R.M.,

Butterfield W.S., Wor
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO96667; AAH96667.1; -; mRNA.
MGI; MGI:96448; Igh-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835, IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
Hypothetical protein_
SEQUENCE 590 AA; 64892 MW; D425318F9A188B14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Muroidea; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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INTERPRO; IPR003599; IG.

INTERPRO; IPR007110; IG-like.

INTERPRO; IPR003597; IG_CI.

INTERPRO; IPR003596; IG_MHC.

INTERPRO; IPR003596; IG_WHC.

INTERPRO; IPR003596; IG_V.

SMART; SM00409; IG; 2.

SMART; SM00400; IG; 2.
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Best Local Similarity 80.0
Matches 8; Conservative
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Search completed: April 25, 2006, 06:24:37 Job time : 55.3962 secs

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April 25, 2006, 06:25:05; Search time 13.4906 Seconds (without alignments) 61.284 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                    572060 segs, 82675679 residues
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Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6_COMB.pep:*
(cgn2_6/ptodata/1/iaa/H_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 110, App Sequence 114, App Description Sequence 1 Sequence Sequence S Sequence US-08-783-853A-84 US-08-783-853A-84 US-08-783-853A-84 US-08-425-336-124 US-08-425-336-125 US-08-425-336-126 US-08-488-113B-124 US-08-477-484B-124 US-08-477-484B-126 US-08-107-669D-29 US-08-107-669D-66 US-08-107-669D-67 US-08-472-788A-29 US-08-472-788A-29 US-08-472-788A-89 US-08-472-788A-89 US-08-472-788A-89 US-08-472-788A-89 US-08-472-788A-89 US-08-472-788A-89 US-08-472-788A-89 US-08-472-788A-89 SUMMARIES Length DB Query Match Score Result

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Gaps

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Query Match
100.0%; Score 58; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels

Sequence 28, Appl Sequence 29, Appl Sequence 89, Appl Sequence 124, App Sequence 126, App Sequence 106, App Sequence 106, App Sequence 108, App Sequence 108		
28 55 94.8 118 1 US-08-082-842A-28 30 55 94.8 118 1 US-08-082-842A-29 31 55 94.8 118 1 US-08-082-842A-88 32 55 94.8 118 1 US-08-082-842A-89 33 55 94.8 118 2 US-08-839-765-124 34 55 94.8 118 2 US-08-839-765-124 35 59 48 118 2 US-09-136-389-124 36 55 94.8 118 2 US-09-136-389-124 37 55 94.8 118 2 US-09-610-838-124 40 55 94.8 118 2 US-09-610-838-124 40 55 94.8 118 2 US-09-11-485-124 41 55 94.8 118 2 US-09-11-485-124 42 55 94.8 118 2 US-09-11-485-124 43 55 94.8 118 2 US-09-11-485-124 44 55 94.8 118 2 US-09-908-469-108 45 59 94.8 118 2 US-08-908-469-108 45 59 94.8 118 2 US-08-908-469-108	ALIGNMENTS RESULT 1 US-08-908-469-110 ; Sequence 110, Application US/08908469	LINFORMATION: PPLICANT: Baca, Manuel Presta, Leonard G. Lownan, Henry B. Chen, Yvonne M. ITLE OF INVENTION: PRESENTION: PRESENTION: PRESENTION: CHEN, Yvonne M. CHEN, BACE G. CHEN, ANTI-VEGF UMBER OF EQUENCES: 131 ORRESPONDENCE ADDRESS: CHENT: 1 DNA MAY CITY: South San Francisc STREET: 1 DNA MAY CITY: South San Francisc COUNTRY: USA ZIP: 94080 OMPUTER READABLE FORM: MEDIUM TYPE: 3: inch, 1 COMPUTER: IBM PC compati OPERATING SYSTEM: PC-DOS SOFTWARE: WIDAMER: US/O FILING DATE: 2-MAY-2001 CLASSIFICATION DATA: APPLICATION NUMBER: US/O FILING DATE: 1-MAY-2001 CLASSIFICATION DATA: APPLICATION NUMBER: US/O FILING DATE: 1-MAY-2001 CLASSIFICATION NUMBER: 08/8 FILING DATE: 1-MAY-2001 CLASSIFICATION NUMBER: 04/4 REFERENCE/DOCKET NUMBER: 44/4 TELEFAM: 650/952-9881 TYRE: AMINO MATA TELEFAM: 650/952-9881 TYRE: AMINO MOS 110: EQUENCE CHARACTERICTICS: LENGTH: 118 amino acids TYPE: Amino Acid

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APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Padlan, Andrew
APPLICANT: Padlan, Rubardo
APPLICANT: PALVESTEIN ANTICOAGULANT AGENTS USBFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.8%; Score 55; DB 2; Length 10; 90.0%; Pred. No. 0.013; 1ive 1; Mismatches 0; Indels
                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windpatin (Genentech) CURRIT APPLICATION NUMBER: US/08/908,469 FILING DATE: 21-May-2001 CLASSIFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION: CUNKNOWN>
RILING DATE: 07-APR-1997
ATTORNEY/AGBRY INFORMATION:
NAME: O1: SF-EVEN X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAME: CLI, Steven X.
REGISTRATION NUMBER: 44,637
REGISTRATION NUMBER: 9109391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-9881
INFORMATION FOR SEQ ID No: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPES Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID No: 1:
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
PEPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
                                                          CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 84, Application US/08783853A Patent No. 6005091 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B: Diskette
IBM Compatible
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Best Local Similarity 90.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1 DNA WAY

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COM
                                                                                                                                                                                                                                                                                                                        APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLI, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
                                                                                                                                                                                                                           Sequence 114, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 118 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100
Matches 10; Conservative
1 GYTFTNYGIN 10
                                  26 GYTFTNYGIN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYTFTNYGIN 10
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                                                                                                                                                                                                   US-08-908-469-114
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Gaps

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APPLICANT: Blackburn, Michael
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padian, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
APPLICANT: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55; DB 2;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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MEDIUM TYPE: Diskette
COMPUTER: Diskett
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUT
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; Sequence 20, Application US/08783853A
Patent No. 6005091
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
                                                                                                                              84:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.8%;
                                                                                                                 INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal
CRIGINAL SOURCE:
US-09-344-050-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GYTFTNYGMN 12
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USA
                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
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APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Church, Witchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Padlan, Eduardo
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.8%; Score 55; 90.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: EM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastERQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
CLASSIFICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumetater, Kirk
REGISTRATION NUMBER: 33,833
REGISTRATION NUMBER: 33,833
            CLASSIPICATION:
PROOF APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
PILING DATE: 24-OCT-1996
ATTONEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REPERRACE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 84, Application US/09344050 Patent No. 6391299
                                                                                                                                                                                                                                                                                                                                                                                          84:
                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHRACTERISTICS:
LENGTH: 92 amino acida
TYPE: amino acida
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-783-853A-84
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Gaps

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Sequence 124, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Proceins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: MARTHALI O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                        94.8%; Score 55; DB 2; Length 112; 90.0%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.8%; Score 55; DB 1; Length 118; 90.0%; Pred. No. 0.15; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESS...
ADDRESS...
STREET: 630.
CITY: Chicago
STRATE: 11Jiniois
COUNTY: USA
ZIP: 6606-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: Batenin Release #1.0, Version #1.25
SOFTWARE: Patenin Release #1.0, Version #1.25
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION NUMBER: US 07/901,707
PILING DATE: 19-MA-1993
PRILING DATE: 19-MA-19
                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Owery Match
Best Local Similarity 90.0.
The second of the 
                            Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                     1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GYTPTNYGIN 10
                                                                                                                                                                                                                                                                    23 GYTFTNYGMN 32
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                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-08-425-336-124
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                                                                                                                                                                                                                                                                                                                                                      94.8%; Score 55; DB 2; Length 112; 90.0%; Pred. No. 0.14; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia RATE: PA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19406
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEX Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUBBER: 08/783,853
PILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-783-853A-20
                                                                                                                                                                                                                                                                                                                                                      Query Match 94.8
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal
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STRANDEDNESS: single
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 GYTFTNYGMN 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYTFTNYGIN 10
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; ORIGINAL SOURCE:
US-09-344-050-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
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Gaps
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Sequence 126, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSER: MCANDAGEWS, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                           CALP: 0.000.1

CALP: 0.000.1

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,1138
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/425,336
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/64,691
PILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/064,691
PILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
PILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
PILING DATE: 04-NOV-1991
ATTONEY/AGENT INPORMATION:
ANAMO: ANAMO: ADARE MANAMO: ANAMO: ANAMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GYTFTNYGIN 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                   Illinois
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                               60661
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Sequence 124, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Setter, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSES: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
Sequence 126, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Proceins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARSHAll, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                            CITY:
STATE: Illia...
COUNTRY: USA
ZIP: GOGGG-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREADTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIPICATION NUMBER: 08/064,691
FILING DATE: 12-MX-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-50.989
RESERRENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION NUMBER: 312/474-6300
TELECHONE: 312/474-6300
TELECHONE: 312/474-6300
TELECHONE: ARS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.8%;
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Best Local Similarity 90.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                             STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-08-488-113B-124
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 GYTFINYGMN 35
                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-477-484B-124
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| Sequence 124, Application US/08477484B
| Sequence 124, Application US/08477484B
| Patent No. 575663B
| Patent No. 575663B
| Patent No. 576663B
| APPLICANT: Better, Marc D. APPLICANT: Studnika, Gary M. Better Studnika, Gary M. ITILE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins | TITLE OF INVENTION: | TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION NUMBER: US 08/64,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-DUN-1992
PRIOR APPLICATION NUMBER: US 07/981,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: US-DUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: US-DUN-1992
RICK APPLICATION NUMBER: US 07/787,567
FILING DATE: US-DUN-1992
RICK APPLICATION NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION NUMBER: 31,918
REGISTRANCE/DOCKET NUMBER: 11022US07/200-70.P3.CZA
TELECOMMUNICATION NUMBER: 31,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.CZA
TELECOMMUNICATION NUMBER: 31,918
TELEDRAK: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11022US07/200-70.P3.C2A
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 1,
Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 GYTFTNYGMN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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| PRICESTFICATION | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190
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Sequence 29, Application US/08107669D

Sequence 29, Application US/08107669D

Patent No. 576686

GENERAL INFORMATION:
APPLICANT: Studincka, Gary M.
TITLE OF INVERTION: Modified Antibody Variable Domains (as amended)
TITLE OF INVERTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STREET: D.C.
COUNTRY: United States of America
STATE: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 0.15;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                Length 118;
                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elem PC compactible
COMPUTER: TEM PC compactible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,669D
PILING DATE: 13-AUG-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
PILING DATE: 14-DEC-1992
PRICH APPLICATION DATA:
APPLICATION NUMBER: BCT/US92/10906
PILING DATE: 11-DEC-1992
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 11-DEC-1991
REGISTRATION NUMBER: 33,851
REGISTRATION NUMBER: 33,851
REGISTRATION NUMBER: 0610.1000001/MAC
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                         Score 55; DB 1;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                       TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 29:
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amino acid
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GYTFTNYGIN 10
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Best Local Similarity
Matches 9; Conserv
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US-08-107-669D-29
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US-08-107-669D-28
Sequence 28, Application US/08107669D
Patent No. 576686
GENERAL INFORMATION:
INFORMATION:
APPLICANT: Studnicka, Cary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
MUMBER OF SEQUENCES:
ADDRESSER: Sterne, Kessler, Goldstein and Pox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,669D
FILING DATE: 13-AUG-1993
CLASSIFICATION NUMBER: BC-1993
FILING DATE: 14-DEC-1993
FILING DATE: 13-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.8%; Score 55; DB 1; Length 118; 90.0%; Pred. No. 0.15;
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     PILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
PULING DATE: 12-MAY.1993
PRIOR APPLICATION DATA:
PILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
PILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
PRIOR APPLICATION NUMBER: US 07/787,567
PRIOR APPLICATION NUMBER: 32,918
PREPERROR DOTE: 32,918
PREPERROR DOTE: 32,918
PREPERROR DOTE: 32,918
PREPERROR DOTE: 312/707-8889
TELERAX: 5312/707-8889
TELERAX: 5312/707-9155
TELERAX: 5312/707-9155
TELERAX: 650 388-1248
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LENGTH: 118 amino acids
TYPE: amino acid
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Best Local Similarity 90.0
Matches 9; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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RESULT 14

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Search completed: April 25, 2006, 06:28:38 Job time : 13.4906 secs

OM protein

Run on:

Sequence:

Searched:

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Sequence 110, Application US/09056160B
Fatent No. US20000032115A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Chen, Yoone M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYTFTNYGIN 10
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US-09-056-160B-110
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FEATURE:
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112, App
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10, App
11, App
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                                                                                   April 25, 2006, 06:58:17; Search time 43.5849 Seconds (without alignments) 95.866 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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                                                                                                                                                                                                                                                                                                                                                                  Published Applications AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-056-160B-114
US-10-234-671-108
US-10-234-671-102
US-10-234-671-112
US-10-974-591-102
US-10-974-591-102
US-10-974-591-102
US-10-974-291-102
US-10-764-428-27
US-10-764-428-27
US-10-764-428-27
US-10-764-428-27
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US-10-76-852-10
US-10-76-852-10
US-10-76-852-10
US-10-76-852-10
US-10-76-852-10
US-10-78-434-115
US-10-78-434-116
US-10-243-130-19
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                                                                                                                                                                                                                          1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            protein search, using sw model
                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Result

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Sequence 14, Application US/10764428

Sequence 14, Application No. US20040229310A1

GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
TITLE OF INVENTION: TIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
TITLE OF INVENTION: CULTURE
TITLE OF INVENTION NUMBER: US 60/442,484

PRIOR FILING DATE: 2003-01-23

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 14

LENGTH: 10
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Sequence 1
Sequence 2
Sequence 4
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Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 10; Conservative 0; Mismatches 0; Indels
US-09-965-099-84
US-10-051-852-84
US-10-681-421-84
US-09-965-099-20
US-10-681-421-84
US-10-681-421-84
US-10-830-899-50
US-10-830-899-50
US-10-830-899-50
US-10-831-899-50
US-10-861-662-50
US-10-861-662-50
US-10-861-662-50
US-09-971-543-8
US-09-971-543-10
US-09-971-543-10
US-09-971-543-10
US-09-971-543-10
US-09-971-543-10
US-09-971-543-10
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US-10-764-428-14
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Query Match 100.0%; Score 58; DB 4; Length 118; Best Local Similarity 100.0%; Pred. No. 0.094; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                      100.0%; Score 58; DB 3; Length 118; 100.0%; Pred. No. 0.094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/234,671
FILLING DATE: 03-88P-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 09/056160
APPLICATION NUMBER: 00/126446
FILLING DATE: 07-APR-1997
APPLICATION NUMBER: 60/12646
FILLING DATE: 06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P1093R2C1
                                                                                                                                                                                                              0; Mismatches
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TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-234-671-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 44,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 108, Application US/10234671
Publication No. USZ0030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEPAR: 650/952-9881
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 118 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                      TYPE: Amino Acid
TOPOLOGY: I'd
  650/225-1896
                                                                                                                                                                                            Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                    1 GYTFTNYGIN 10
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TELEPHONE:
TELEFAX: 6
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genetecch) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/056,160B FILING DATE: 06-AQT-1998 CLASSIFICATION NATA: APPLICATION NATA: APPLICATION NATA: APPLICATION NATA: APPLICATION NATA: APPLICATION NATA: APPLICATION NATE: 06-AUG-1997 ATOKNEY/AGENT INFORMATION: NAME: Haeak, Janet E. REGISTRATION NUMBER: 28,616 REFERENCE/DOCKET NUMBER: 28,616 REFERENCE/DOCKET NUMBER: P1093R2 TELECOMMUNICATION INFORMATION:
                ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-APP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 114, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
PAPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GYTFTNYGIN 10
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US-09-056-160B-110
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    COUNTRY:
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100.0%; Score 58; DB 5; Length 118; 100.0%; Pred. No. 0.094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1EM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winpatin (Genentech) CURRENT APPLICATION DATE: APPLICATION NUMBER: US/10/974,591 PILING DATE: 26-Oct-2004 CLASSIFICATION OF COMPUTER: OP/723752 APPLICATION NUMBER: 09/723752
                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 58; DB 5; Best Local Similarity 100.0%; Pred. No. 0.094; Matches 10; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTI-BODIES
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P1093P1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 108: US-10-974-591-108
CURRENT APPLICATION NUMBER: US/10/683,043
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/218,481
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 27-NOV-2000
APPLICATION NUMBER: 08/908469
PILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/833504
PILING DATE: 07-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 108, Application US/10974591
Publication No. Us20050112126A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-683-043-11
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                                                                                                                                                                            SEQ ID NO 11
LENGTH: 118
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Sequence 11, Application US/10683043

Sequence 11, Application US/005053599A1

PUBLICANT VORMATION:
APPLICANT: Van Bruggen, Nicholas

APPLICANT: Perrara, Napoleone

TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists

TITLE OF INVENTION: and Uses Thereof

FILE REFERENCE: P1717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER TALABLE FORM:
COMPUTER: 15.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: CUbknown.
PRIOR APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-ANG-1997
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100.0%; Pred. No. 0.094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 13:
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CLi, Steven X.
REGISTRATION NUMBER: 44,637
REPERENCE/POCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-9814
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
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SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-234-671-112
                                                                                                                                                                                                               Sequence 112, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                             Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
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Matches 10; Conservative
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                    -10-234-671-112
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JS-10-764-428-5
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Publication No. US20050048572A1;
GENERAL INFORMATION:
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
ODRUTISE: 1BM PC compatible
ODREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 26-OCt-2004
CIASSIPTCATION NUMBER: 09/723752
FILING DATE: 7-NOV-2000
APPLICATION NUMBER: 09/723752
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/908469
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/908469
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 08/833504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cul, Steven X.
REFERENCE/DOCKET NUMBER: 91093PIDICI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                           Sequence 112, Application US/10974591
Publication No. US20050112126A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
COMEN, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 112: US-10-974-591-112
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 650/225-8674
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
COUNTRY: USA
                    26 GYTFINYGIN 35
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GYTPINYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
                                                                                                                                  US-10-974-591-112
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                                                                                                         RESULT 8
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; OTHER INFORMATION: The first 214 amino acids are the light chain followed by the ; OTHER INFORMATION: heavy chain beginning at position 215 (E).
US-10-764-428-5
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Sequence 9, Application US/10764428
Publication No. US20040229310A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
TITLE OF INVENTION: YIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
TITLE OF INVENTION: CULTURE
FILE REFERENCE: 11669.120USU1
CURRENT FAPLICATION NUMBER: US/10/764,428
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/442,484
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10764428
Sequence 5, Application US/10764428
Publication No. US20040229310A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
TITLE OF INVENTION: TIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
TITLE OF INVENTION: CULTURE
FILE REFERENCE: 11669.120USU1
CURRENT APPLICATION NUMBER: US/10/764,428
CURRENT FILING DATE: 2004-01-23
FRIOR APPLICATION NUMBER: US 60/442,484
PRIOR FILING DATE: 2003-01-23
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Pred. No. 0.36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
FILE REFERENCE: 11669.195USU1
CURRENT APPLICATION NUMBER: US/10/697,995
CURRENT FILING DATE: 2003-10-30
FRIOR APPLICATION NUMBER: US 60/422,952
PRIOR FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 12
LENGTH: 479
TYPE: PRI
                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Anti-VEGF heavy chain US-10-697-995-12
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0
                                                                                                                                                                                                                                                                  ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 GYTFTNYGIN 249
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US-10-764-428-11

Sequence 11, Application US/10764428

Publication No. US20040229310A1

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING

TITLE OF INVENTION: WITLE OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL

TITLE OF INVENTION: CULTURE

TITLE OF INVENTION: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Light chain starts at residue 1 (D); Heavy chain starts at ; OTHER INFORMATION: residue 215 (Q)
US-10-764-428-11
                                                                                                                                                                                                                                                               OTHER INFORMATION: Light chain starts at residue 1 (D); Heavy chain starts at OTHER INFORMATION: residue 215 (Q)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 58; DB 5; Length 670; 100.0%; Pred. No. 0.49;
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100.0%; Pred. No. 0.49;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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ORGANISM: Artificial Sequence
PEATURE:
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ORGANISM: Artificial Sequence
Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100 Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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; OTHER INFORMATION: Light chain starts at residue 1 (D); Heavy chain starts at; OTHER INFORMATION: residue 215 (Q)
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Sequence 2, Application US/10706852

Publication No. US20040219203A1

GENERAL INFORMATION:

APPLICANT: GRIFFITHS, GARY L.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: HANSEN, HANS J.

PILE REPERENCE, BO B.

TITLE OF INVENTION: ANTI-CD74 IMMUNOCONJUGATES AND METHODS

FILE REPERENCE, 10023-0079US5

CURRENT PILING DATE: 2003-11-12

PRIOR PELICATION NUMBER: 09/965,796

PRIOR PILING DATE: 2002-10-01

PRIOR PILING DATE: 2003-10-01

PRIOR PILING DATE: 2003-01-24

PRIOR PILING DATE: 2003-03-03

PRIOR PILING DATE: 2003-04-04

PRIOR PILING DATE: 2003-03-03

PRIOR PILING DATE: 2003-03-03

PRIOR PILING DATE: 2003-04-04

PRIOR PILING DATE: 2003-04-04

PRIOR PILING DATE: 2003-06-17

PRIOR APPLICATION NUMBER: 60/478,830

PRIOR PILING DATE: 2003-06-17

PRIOR PILING DATE: 2003-06-17

PRIOR PILING DATE: 2003-06-17

PRIOR PILING DATE: 2003-06-17
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Sequence 6, Application US/10706852
Sequence 6, Application No. US20040219203A1
GENERAL INPORMATION:
APPLICANT: GARTIFFITHS, GARY L.
APPLICANT: HANSEN, HANS J.
APPLICANT: LUNDBERG, BD
TITLE OF INVENTION: ANTI-CD74 IMMUNOCONJUGATES AND METHODS
FILE REFERENCE: 40923-0079US5
CURRENT APPLICATION NUMBER: US/10/706,852
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 10/314,330
                                                                                                                                 Query Match
100.0%; Score S8; DB 5; Length 670;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels
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90.0%; Pred. No. 0.14;
tive 1; Mismatches (
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Best Local Similarity 90.v.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                              240 GYTFTNYGIN 249
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US-10-706-852-2
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PRIOR FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 09/965,796
PRIOR APPLICATION NUMBER: 09/307,816
PRIOR APPLICATION NUMBER: 09/307,816
PRIOR PILING DATE: 1999-05-10
PRIOR PILING DATE: 1999-05-10
PRIOR PILING DATE: 2003-01-24
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-01
PRIOR PELING DATE: 2003-03-01
PRIOR PILING DATE: 2003-06-17
PRIOR PILING DATE: 2003-06-17
PRIOR PILING DATE: 2003-06-17
NUMBER OF EGQ ID NOS: 21
SOFTWARE: PATENTIN VET: 3.2
SOFTWARE: PATENTIN VET: 3.2
SOFTWARE: PATENTIN VET: 3.2
PRIOR PILING DATE: 2003-06-17
NUMBER OF EGG ID NOS: 21
PRIOR PILING DATE: 2003-06-17
NUMBER OF EGG ID NOS: 21
PRIOR PILING DATE: 2003-06-17
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PRIOR PILING DATE: 2003-06-17
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PRIOR PILING DATE: 2003-06-17
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PRIOR PILING DATE: 2003-06-17
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PRIOR PILING DATE: 2003-06-17
NUMBER OF EGG ID NOS: 21
PRIOR PILING DATE: 2003-01
PRIOR PILING DATE: 
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98.3%; Score 57; DB 5; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 1; Mismatches 0; Indels
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26 GYTFTNYGVN 35
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Search completed: April 25, 2006, 07:08:46 Job time : 44.5849 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                      April 25, 2006, 07:01:21 ; Search time 6.41509 Seconds (without alignments) 68.593 Million cell updates/sec
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1: /SIDS5/ptodata/1/pubpaa/US06_NEW_FUB.pep:*

2: /SIDS5/ptodata/1/pubpaa/US07_NEW_FUB.pep:*

3: /SIDS5/ptodata/1/pubpaa/US07_NEW_FUB.pep:*

5: /SIDS5/ptodata/1/pubpaa/PCT_NEW_FUB.pep:*

5: /SIDS5/ptodata/1/pubpaa/US07_NEW_FUB.pep:*

7: /SIDS5/ptodata/1/pubpaa/US10_NEW_FUB.pep:*

7: /SIDS5/ptodata/1/pubpaa/US11_NEW_FUB.pep:*

8: /SIDS5/ptodata/1/pubpaa/US11_NEW_FUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                            US-10-764-428-14
58
                                                                                                                                                                                                                                                                                                                                                   1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                               Title:
Perfect score:
Sequence:
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SUMMARIES

		•			SUMMAKIES		
Result No.	Score	* Query Match	* Query Match Length DB	DB	ID	Description	
1	58	100.0	118	و ا	US-10-648-816-11	Sequence 11, Appl	
100	55	94.8	92	7	US-11-240-195-84		
· M	55	94.8	112	7	US-11-240-195-20	Sequence 20, Appl	
4	55	94.8	116	7	US-11-174-186-2	~	
ហ	55	94.8	116	7	US-11-174-186-4	4	
9		94.8	116	7	US-11-174-186-6	6, 1	
7	55	94.8	116	7	US-11-174-186-17	17,	
80	55	94.8	116	7	US-11-174-186-18	18,	
o	55	94.8	116	7	US-11-174-186-19	19,	
10	55	94.8	116	7	US-11-174-186-20	20,	
11	55	94.8	116	7	US-11-174-186-21	21,	
17	55	94.8		7	US-11-174-186-22	22,	
13	55	94.8	116	7	US-11-174-186-23	23,	
14	55	94.8	116	7	US-11-174-186-24	24,	
15	55	94.8	•	7	US-11-174-186-25	25,	
16	55	94.8	116	7	US-11-174-186-26	56	
17	55	94.8	117	7	US-11-174-186-35	35,	
18	55	94.8	117	7	US-11-037-199-32	32	
19	55	94.8	118	9	US-10-648-816-9	ο	
20	55	94.8	118	9	US-10-648-816-14	14	
21	55	94.8	121	9	US-10-648-816-15	Sequence 15, Appl	
22	55	94.8	121	7	US-11-240-195-7	Sequence 7, Appli	
23	55	94.8	121	7	US-11-240-195-31	3	
24	55	94.8	121	7	US-11-240-195-52	52,	
25	55	94.8	121	7	US-11-240-195-111	Sequence 111, App	

Sequence 109, App Sequence 8, Appli Sequence 10, Appl Sequence 89, Appl	48222	466644	Sequence 1897, Ap Sequence 2078, Ap Sequence 1897, Ap Sequence 2078, Ap Sequence 1530, Ap
7 US-11-240-195-109 7 US-11-208-422-8 7 US-11-208-422-10	11-174-186- 11-054-515- 11-054-515- 11-054-515-	7 US-11-266-444-11885 1 US-11-266-444-2124 1 US-11-266-444-2126 1 US-11-266-444-2127 1 US-11-266-444-1008	7 US-11-054-515-1897 7 US-11-054-515-2078 7 US-11-266-444-1897 7 US-11-266-444-2078 7 US-11-054-515-1530
		22222 44222 744444 7778	
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,	53 91.4 53 91.4 53 91.4 53 91.4	91.4 91.4 91.4 91.4
22 23 24 28	3 3 3 3 3 4 3 5 4 5 5 5 5 5 5 5 5 5 5 5	# B B B B B B B B B B B B B B B B B B B	44444

ALIGNMENTS

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APPLICANT: Van Bruggen, Nicholas
APPLICANT: Van Bruggen, Nicholas
APPLICANT: Van Bruggen, Napoleone
TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
FILE BEPERSKUE: P1717D1
CURRENT PLING DATE: 2003-08-26
PRIOR PILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 09/718,694
PRIOR PILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 16
SEQ ID NOS: 16
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Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0; Indels
US-10-648-816-11
Sequence 11, Application US/10648816
Publication No. US/0050244405A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                            , ORGANISM: Homo sapiens
US-10-648-816-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-240-195-84
                                                                                                                                                                                                                                                               LENGTH: 118
TYPE: PRT
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Sequence 2, Application US/11174186
Publication No. US20050244418A1
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           23 GYTFTNYGMN 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial
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APPLICANT: Fencration:

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT

TITLE OF INVENTION: OF THROMBOSIS

FILE REFERENCE: FOOLS.

CURRENT APPLICATION NUMBER: US/11/240,195

CURRENT APPLICATION NUMBER: US/11/430,176

PRIOR APPLICATION NUMBER: US/10/430,176

PRIOR PILING DATE: 2003-05-05

PRIOR PILING DATE: 2003-05-05

PRIOR FILING DATE: 2003-05-05

PRIOR PILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/359,202

PRIOR PILING DATE: 1998-08-07

PRIOR PILING DATE: 1999-08-07

PRIOR PILING DATE: 1997-01-06

PRIOR PIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.8%; Score 55; DB 7; Length 92; 90.0%; Pred. No. 0.016; Live 1; Mismatches 0; Indels
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/095,714
PRIOR APPLICATION NUMBER: 10/051,714
PRIOR APPLICATION NUMBER: 10/051,852
PRIOR PELING DATE: 1998-08-07
PRIOR PILING DATE: 2002-01-17
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-01-06
PRIOR PILING DATE: 1996-01-17
PRIOR PILING DATE: 1996-10-24
NUMBER OF SEQ ID NOS: 111
SOFTWARE: FRAEESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/11240195
Publication No. US20060057140A1
GENERAL INFORMATION:
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-11-240-195-84
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LENGTH: 92
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1 GYTFINYGIN 10

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Sequence 4, Application US/11174186

Sequence 4, Application US/11174186

Publication No. US20050244418A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Gillies, Stephen
APPLICANT: Gillies, Recombinant Tumor Specific Antibody And Use Thereof
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX.019
CURRENT FILING DATE: 2005-07-01
FRICH APPLICATION NUMBER: US 60/288,564
FRICH RILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 116
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LOCATION: (2). \( (2) \). \( (2) \)
OTHER INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (9). (9). ornania (9). sa at position 9 is a proline or an alanine
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Gil, Kin-Ming
APPLICANT: Gil, Kin-Ming
APPLICANT: Gil, Kin-Ming
APPLICANT: Li, Kin-Ming
FILE REPERENCE: LEX-Oil
FILE REPERENCE: LEX-Oil
FILE REPERENCE: LEX-Oil
FILE PRICE PRICE 2001-05-07
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PARCELIN Version 3.3
SEQ ID NO 2
LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (11)..(11)
OTHER INFORMATION: wherein Xaa at position 11 is a leucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEATURE:
OTHER INFORMATION: variable heavy chain sequence in the EpCAM antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 7; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.8%; Score 55; DB 7; Best Local Similarity 90.0%; Pred. No. 0.02; Matches 9; Conservative 1; Mismatches
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LOCATION: (16)..(16)
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NAME/KBY: misc feature
LOCATION: (100)..(100)
OTHER INFORMATION: wherein Xaa at position 100 is an isoleucine or a methionine
                                                                                                                                                                                                                                                                                LOCATION: (917...(91)
OTHER INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (1087..(108)
OTHER INFORMATION: wherein Xaa at position 108 is a glutamine or a threonine
                                                                                                                                     NAME/KBY: misc_feature
LOCKRION: (88)..(88)..(88)..ksy contrain Xaa at position 88 is an asparagine, an alanine
OTHER INFORMATION: werine
                                                      LOCATION: (85)..(85)
OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature; LOCATION: (111)...(111); OTHER INFORMATION: wherein Xaa at position 111 is a serine or a threonine US-11-174-186-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (2). (2)
OTHER INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (93)...(93)
OTHER INFORMATION: wherein Xaa at position 93 is a threonine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (9).7(9)
OTHER INFORMATION: wherein Xaa at position 9 is a proline or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGS-11-174-186-6
Sequence 6, Application US/11174186
Sequence 6, Application US/11174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Oilan, Xiugi
APPLICANT: OILange APPLICATION NUMBER: US/11/174,186
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR APPLICATION NUMBER: US 60/288,564
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Pred. No. 0.02;
1; Mismatches
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 116
TYPE: PRT
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Best Local Similarity 90.0
Matches 9; Conservative
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NAME/KEY: misc_feature
LOCATION: (11).(11)
                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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LOCATION: (69)...(69)
OTHER INPORMATION: wherein Xaa at position 69 is an alanine, a threonine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TION: (73)...(73)
R INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (70) ... (70)
OTHER INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAMB/KEY: misc_feature
LOCATION: (80) ... (80)
OTHER INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /KEY: msic_feature
TION: (63) ... (63)
R INPORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (68)...(68)
OTHER INFORMATION: wherein Xaa at position 68 is a phenylalanine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAWE/KEY: misc feature
LOCATION: (46)...(46)
OTHER INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
DIMER INFORMATION: wherein Xaa at position 16 is a glutamic acid or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (84)...(84)
OTHER INPORMATION: wherein Xaa at position 84 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (76)...(76)
OTHER INFORMATION: wherein Xaa at position 76 is an alanine or a threonine
                                                                                                                                                                                                                                                                                                                             LOCATION: (40)..(40)
OTHER INFORMATION: wherein Xaa at position 40 is a threonine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (79)...(79)
OTHER INFORMATION: wherein Xaa at position 79 is an alanine or a leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (72)...(72)
OTHER INFORMATION: wherein Xaa at position 72 is a leucine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (65)..(65)
OTHER INFORMATION: wherein Xaa at position 65 is a lysine or a glutamine
                                                                                          LOCATION: (17). (17)
OTHER INFORMATION: wherein Xaa at position 17 is a threonine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                ION: (43)...(43)
INPORMATION: wherein Xaa at position 43 is a lysine or a glutamine
                                                                                                                                                                                                                ION: (38)..(38)
INFORMATION: wherein Xaa at position 38 is a lysine or an arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ON: (83). (83) INFORMATION: wherein Xaa at position 83 is an isoleucine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (73)..(73)
                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
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LOCATION: (40)..(40)
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                                       FEATURE:
NAME/KEY: misc_feature
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FEATURE:

NAME/KEY: misc feature

LOCATION: (108)...(108)

OTHER INFORMATION: wherein Xaa at position 108 is a glutamine or a threonine US-11-174-186-6
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Sequence 17, Application NS/20050244418A1

Sequence 17, Application No. US20050244418A1

GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Gillies, Stephen
APPLICANT: Gillies, Kiugi
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019

CURRENT FILING DATE: 2005-07-01
FRIOR APPLICATION NUMBER: US 60/288,564
FRIOR APPLICATION NUMBER: US 60/288,564
FRIOR PRIOR DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 17
LENGTH: 116
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Sequence 18, Application WS/11174186

Publication No. US20050244418A1

GENERAL INFORMATION:

APPLICANT: Gillies, Stephen

APPLICANT: Gillies, Stephen

APPLICANT: Gillies, Stephen

APPLICANT: Gillies, Stephen

TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof

FILE REPERENCE: LEX-019

CURRENT APPLICATION NUMBER: US/11/174,186

CURRENT FILING DATE: 2005-07-01

PRIOR APPLICATION NUMBER: US 60/288,564

PRIOR RILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.3

SEQ ID NO 18
OTHER INFORMATION: wherein Xaa at position 93 is a threonine or a valine
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Pred. No. 0.02;
1; Mismatches 0; Indels
                                                                                                                                                                                Length 116;
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                                                                                                                                                                                Score 55; DB 7;
Pred. No. 0.02;
1; Mismatches
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, OTHER INFORMATION: VH7 heavy chain
US-11-174-186-18
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ION: (70)... (70)
INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ø
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LOCATION: (80)...(80)
JTHER INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ION: (88)...(88)
INFORMATION: wherein Xaa at position 88 is an asparagine, an alanine or
INFORMATION: serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (63)..(63)
OTHER INFORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /KBY: misc_feature
TION: (68)...(68)
R INFORMATION: wherein Xaa at position 68 is a phenylalanine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (91)...(91)
OTHER INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                      ION: (46)...(46)
INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /KEY: misc feature
TION: (83) ... (83)
R INFORMATION: wherein Xaa at position 83 is an isoleucine or a leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (84)..(84)
OTHER INFORMATION: wherein Xaa at position 84 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (85)...(85)
OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /KBY: misc_feature
TION: (69)<sup>-..</sup>(69)
R INFORMATION: wherein Xaa at position 69 is an alanine or a threonine
                                                                                                                                                                                                                                                                                                  ION: (40)...(40)
INFORMATION: wherein Xaa at position 40 is a threonine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ION: (76)...(76)
INFORMATION: wherein Xaa at position 76 is an alanine or a threonine
                                                                                                               OTHER INFORMATION: wherein Xaa at position 17 is a threonine or a serine
                                                                                                                                                                                                                   arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (65)...(65)
OTHER INFORMATION: wherein Xaa at position 65 is a lysine or a glutamine
          OTHER INFORMATION: wherein Kaa at position 11 is a leucine or a valine
                                                                                                                                                                                                                      an
                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (38)...(38)
OTHER INFORMATION: wherein Xaa at position 38 is a lysine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
rocation: (63)..(63)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (93)..(93)
                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_featrue
LOCATION: (46)..(46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEY: misc_feature
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ORGANISM: Artificial
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US-11-174-186-23
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                                                                                                                                                                                       Sequence 19, Application US/11174186
; Sequence 19, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INPORMATION:
APPLICANT: Gillies, Stephen
; APPLICANT: Gillies, Stephen
; APPLICANT: Lay, Aiugi
; APPLICANT: Lax-019
; TITLE OF INVENTION: Recombinant Tumox Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT APPLICATION NUMBER: US 60/288,564
; PRIOR APPLICATION NUMBER: 2005-07-01
; PRIOR PILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-11-14-186-20

US-11-14-186-20

Sequence 20, Application US/11174186

Publication No. US20050244418A1

GENERAL INPORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Gillies, Stephen
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019

CURRENT FILING DATE: 2005-07-01

PRIOR APPLICATION NUMBER: US 60/288,564

PRIOR PLING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.3

LENGTH: 116
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Score 55; DB 7; Length 116;
Pred. No. 0.02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 7; Length 116; Pred. No. 0.02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: VH2.5 heavy chain US-11-174-186-19
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       94.8%;
90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
     Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Sequence 22, Application US/11174186
; Sequence 22, Application No. US20050244418A1
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kill Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; TITLE OF INVENTION: NUMBER: US/11/174,186
; CURRENT PILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; RILNG DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.3
; SEQ ID NOS: 42
; SEQ ID NOS: 42
; TENNOR 11.6
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Sequence 21, Application US/11174186

Publication No. US20050244418A1

GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Gillies, Stephen
APPLICANT: Gillies, Stephen
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
TITLE OF INVENTION WHERE: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR APPLICATION NUMBER: US 60/288,564
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.3
SEQ ID NO 21
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Pred. No. 0.02;
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; OTHER INFORMATION: KS de-immunized VH2
US-11-174-186-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: KS de-immunized VH1
US-11-174-186-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.8%;
Best Local Similarity 90.0%;
Matches 9; Conservative 1
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Search completed: April 25, 2006, 07:10:01 Job time : 7.58176 secs
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US-11-174-186-24
US-11-174-186-24
Sequence 24, Application US/11174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Qillies, Stephen
APPLICANT: Qian, Xiugi
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REPERENCE: LEX-019
CURRENT FILING DATE: 2005-07-01
PRIOR PILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 24
LENGTH: 116
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US-11-174-186-25
Sequence 25, Application US/11174186
Sequence 25, Application Wo. US20050244418A1
GENERAL INFORMATION:
APPLICANT: G111ies, Stephen
APPLICANT: G111ies, Stephen
APPLICANT: G111ies, Stephen
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Lo, Kin-Ming
APPLICANT: Olan, Xiugi
TILLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT PILING DATE: 2005-07-01
FRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.3
SEQ ID NO 23
LENGTH: 116
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Pred. No. 0.02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: KS de-immunized VH3
US-11-174-186-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: KS- deimmunized VH4
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Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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26 GYTFTNYGMN 35
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PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 25
LENGTH: 116
                                                                                                                                                                                         OTHER INFORMATION: KS de-immunized VH5
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                                                                                                                                  TYPE: PRT ORGANISM: Artificial
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Blocceleration Ltd.
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- protein search, using sw model protein Š

April 25, 2006, 06:05:16 ; Search time 53.3962 Seconds (without alignments) 82.286 Million cell updates/sec Run on:

US-10-764-428-18 62 score: Title: Perfect

1 GYDFTHYGMN 10 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2443163 Total number of hits satisfying chosen parameters:

2443163 seqs, 439378781 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

A Geneseq 21:* : geneseqp1980s:* Database :

geneseqp2008:* geneseqp20018:* geneseqp20028:* geneseqp20038:* geneseqp2003bs:* geneseqp20048:* genевефр1990в:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aaw70662 Fab-phage		Abp61231 Anti-VEGF	-		Antib	•	•	Aaw70688 Anti-VEGF	Aaw70682 Anti-VEGF	Aab05900 F(ab)-12	-	Aab13385 Anti-VEGF	Aab13384 Anti-VEGF	App61255 Humanised	Abp61257 Humanised	_	Aab05902 F(ab)-12		-	•	Abp51953 Plasmid p	Abb81110 Anti-VEGF	Adol4129 Plasmid p
er	AAW70662	AAW70698	ABP61231	ABP61267	ADQ90714	ADF09953	ADF10058	AAW70686	AAW70688	AAW70682	AAB05900	AAB13382	AAB13385	AAB13384	ABP61255	ABP61257	ABP61251	AAB05902	AAB13391	ADG31769	AEA40494	ABP51953	ABB81110	AD014129
DB	0	N	Ŋ	ß	œ	,	7	~	N	N	m	m	٣	ო	S	S	ß	m	m	۵	σ	ß	'n	œ
& Query Match Length	10	10	10	10	10	117	117	118	118	118	118	118	118	118	118	118	118	121	121	123	123	254	476	476
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62
Result No.	-	10	· m	4	'n	· w	7	80	0	10	::	12	13	14	15	16	17	18	19	20	21	22	23	24

				Anti-VEGF Anti-VEGF Anti-VEGF Fab-phage Anti-VEGF
Adq90730 Adq90733 Aea40565 Aea40533	Aaw70664 Aaw70666 Abp61233 Abp61235	Aaw70665 Abp61234 Aea40569 Aea40573	Aea17137 Aea40548 Aea40544 Adc26162	Adc26158 Adc26161 Adc26163 Aaw70667 Abp61236
ADQ90730 ADQ90733 AEA40565 AEA40533	AAW70664 AAW70666 ABP61233 ABP61235	AAW70665 ABP61234 AEA40569 AEA40573	AEA17137 AEA40548 AEA40544 ADC26162	ADC26158 ADC26161 ADC26163 AAW70667 ABP61236
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476 476 10	1222	2222	117 123 123 231	231 234 10 10
100.0 100.0 95.2		88.7 88.7 7.88 7.88	88.7 88.7 88.7	88.7 88.7 88.7 87.1
62 2 2 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4				N N N N N N N N T T T
2 2 6 5 2 4 4 5 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3333	1 W W W W	288 40 80 80	4 4 4 4 4 11 52 62 4 53

ALIGNMENTS

AAW70662 ID AAW7

AAW70662 standard; peptide; 10 AA.

AAW70662;

27-JAN-1999 (first entry)

Fab-phage library HL-265 anti-VEGF variant Y0243-1.

Murine; humanised antibody; VEGF-induced angiogenesis; tumour; anti-vascular endothelial growth factor antibody; anti-VEGF antibody; retinal disorder; age-related macular degeneration; diabetic retinopathy; rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

Synthetic.

WO9845331-A2

15-0CT-1998

98WO-US006604. 03-APR-1998;

97US-00833504. 07-APR-1997; 06-AUG-1997;

(GETH) GENENTECH INC.

Chen YM; Lowman HB, Wells JA, Presta LG, Baca M,

WPI; 1998-568337/48.

New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other anglogenic states, also related nucleic acid, vectors and transformed cells.

Example 3; Page 74; 100pp; English.

(anti-VEGF) antibody variants from Pab-phage library HL-265. The sequences are used in the course of the invention to produce the humanised anti-VEGF antibody of the invention to produce the humanised anti-VEGF antibody of the invention. The humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. ageuslated mecular degeneration or diabetic retinopathy). They can also be used to treat other conditions that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

Query Match

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Matches

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AAW70698

AAW70698 ID AAW7 RESULT

Мив вр.

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The present invention relates to humanised anti-VEGF (vascular anti-VEGF antichelal growth factor) antibodies or a variant of a parent anti-VEGF antibody, which binds human VEGF. The anti-VEGF antibodies are useful for inhibiting VEGF-induced angiogenesis in a mammal (particularly a human), particularly those having a tumour or a retinal disorder e.g. intraccular neovascular disorders. The present sequence is a peptide fragment of an anti-VEGF variant from a second generation Fab-phage library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New humanized anti-VEGF (vascular endothelial growth factor) antibodies or their variants, useful for inhibiting VEGF-induced angiogenesis in a mammal, particularly for treating tumor or retinal disorders.
                                                                                                                                                                         Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF; vascular endothelial growth factor; angiogenesis inhibitor; tumour; retinal disorder; intraocular neovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF; vascular endothelial growth factor; angiogenesis inhibitor; tumour; retinal disorder; intraocular neovascular disorder; heavy chain; variable domain; CDRHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised anti-VEGF antibody heavy chain variable domain, CDRH1.
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100.0%; Pred. No. 0.00091;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Presta LG, Lowman HB, Chen YM;
                                                                                                                                    Anti-VEGF antibody VH1 peptide Y0243-1.
                  ABP61231 standard; peptide; 10 AA.
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Query Match
Best Local Similarity 100...
Best Local Similarity 100...
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WELLS J A.
PRESTA L G.
LOWMAN H B.
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                                                                                                                                                                                                                                                                                                US2002032315-A1.
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                                                                                                                                                                                                                                                                                                                                                                             06-APR-1998;
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                                                                                                20-SEP-2002
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                                                                                                                                                                                                                                                           Synthetic.
                                                           ABP61231;
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ABP6123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                  Heavy chain hypervariable region; murine; humanised antibody; anti-vascular endothelial growth factor antibody; anti-VEGF antibody; VEGF-Induced angiogenesis; tumour; retinal disorder; agge-related macular degeneration; diabetic retinopathy; rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
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                                     100.0%; Score 62; DB 2; Length 10; 100.0%; Pred. No. 0.00091;
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100.0%; Pred. No. 0.00091;
ive 0; Mismatches 0; Indels
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97US-00908469
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hes 10; Conservative
                                                         Local Similarity 100.
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  Sequence 10 AA;
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06-AUG-1997;
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Gaps

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Query Match

Matches

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The present invention relates to humanised anti-VEGF (vascular endothelial growth factor) antibodies or a variant of a parent anti-VEGF antibody, which binds human VEGF. The anti-VEGF antibodies are useful for inhibiting VEGF-induced angiogenesis in a mammal (particularly a human), particularly those having a tumour or a retinal disorder e.g. intraocular neovascular disorders. The present sequence is an exemplary heavy chain variable domain of the humanised anti-VEGF antibody of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New humanized anti-VEGF (vascular endothelial growth factor) antibodies or their variants, useful for inhibiting VEGF-induced angiogenesis in a mammal, particularly for treating tumor or retinal disorders.
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100.0%; Pred. No. 0.00091;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowman HB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ90714 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 23; Page 31; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Presta LG,
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nes 10; Conservative
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WELLS J A.
PRESTA L G.
LOWMAN H B.
CHEN Y M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-517920/55.
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                                                                                                                                       US2002032315-A1
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                           Homo sapiens
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                                                   Mus sp.
Synthetic.
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(WELL/)
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(LOWM/)
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Matches
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ADQ90714
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Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework
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                                                                                                                                                                                                                                                                          100.0%; Score 62; DB 8; Length 10; 100.0%; Pred. No. 0.00091;
                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Antibody heavy chain variable region 1CZ8(7-4-1).
                                                                                                                                                                                                                                                                                      Mismatches
                                                                              Claim 13; SEQ ID NO 18; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                ADF09953 standard, protein; 117 AA.
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     23-JAN-2003; 2003US-0442484P.
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Matches 10; Conservative
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                                                                  region in a host cell
                 (GETH ) GENENTECH INC
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                                         WPI; 2004-562149/54.
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                              Simmons L;
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method. The method comprises of a manibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the acid at each variable position with at least part of the remainded at the acid at each variable position with at least part of the remainder of the antibody, including the selected amino acid at other variable position with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical property. The method is useful for optimizing the physico-chemical property. The method is useful for optimizing the physico-chemical property. The present sequence with at least one solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody wariable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a variable heavy domain of an affinity-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-VEGF humanised antibody variable heavy domain of variant Y0313-1
                                                                                             The present invention relates to a method for optimizing at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heavy variable domain; murine; humanised antibody;
anti-vascular endothelial growth factor antibody; anti-VEGF antibo
VEFF-induced anglogenesis; tumour; retinal disorder;
age-related macular degeneration; diabetic retinopathy;
rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
comprises analyzing the interactions of amino acids at variable positions.
                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 62; DB 7; Length 117; 100.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW70686 standard; peptide; 118 AA.
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                                                           Example 6; Fig 16a; 135pp; English
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                           Sequence 117 AA;
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06-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW70686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baca M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                  physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one enforced belonging to the antibody structure; selecting at least one enforced belonging to the antibody structure; selecting at least one enforced to be considered at the variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical property of an antibody, especially the stability, solubility, or antigen binding affinity. The optimized may be useful for treating a patient. The present sequence is an antibody may be variable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                       present invention relates to a method for optimizing at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                        Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer optimization of physicochemical properties of antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 62; DB 7; Length 117; 100.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    solubility; antigen binding affinity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                Dahiyat B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dahiyat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF antibody heavy chain variable region 1CZ8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                Marshall SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desjarlais JR, Marshall SA,
                                                                                                                                                                                                                                                       Disclosure; Fig 2a; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADF10058 standard; protein; 117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAR-2003; 2003WO-US006598.
                            01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variable region; human; VEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                Desjarlais JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYDFTHYGMN 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody; stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-722066/68.
                                                                                                                                                 WPI; 2003-722066/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003074679-A2
                                                                                (XENC-) XENCOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2003
                                                                                                                Lazar GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lazar GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
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Chen YM;

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Gaps

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0; Indels

Query Match

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The present sequence represents a variable heavy domain of an affinity-matured anti-vascular endothelial growth factor (anti-VBGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VBGF antibody of the invention. The humanised anti-VBGF antibody of the invention. The humanised for treating or preventing tumours (of any type) and retinal disorders for treating or preventing tumours (of any type) and retinal disorders also be used to treat other conditions that involve anglogenesis, e.g.
                                                                                                                                                                                                                         ö
matured anti-vascular endothelial growth factor (anti-VEGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinopathy). They can also be used to treat other conditions that involve angiogenesis, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.
                                                                                                                      rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy variable domain; murine; humanised antibody; anti-VEGF antibody; anti-vascular endothelial growth factor antibody; anti-VEGF antibody; VEGF-induced angiogenesis; tumour; retinal disorder; age-related macular degeneration; diabetic retinopathy; rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-VEGF humanised antibody variable heavy domain of variant Y0317.
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                                                                                                                                                                                       100.0%; Score 62; DB 2; Length 118; 100.0%; Pred. No. 0.011;
                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 AAW70688 standard; peptide; 118 AA.
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                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                GYDPTHYGMN 35
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                                                                                                                                                                                                                                                              GYDPTHYGMN
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                                                                                                                                                                                                           Similarity
10; Conserv
                                                                                                                                                           Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAW70688
                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                              RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.
                                                                                                                                                                                                                                                     Anti-VEGF humanised antibody variable heavy domain of variant Y0243-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                 anti-VEGF antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanised antibody with affinity for vascular endothelial growth
                               Gape
                                                                                                                                                                                                                                                                            Heavy variable domain; murine; humanised antibody; anti-VEGF antibo VEGF-induced angiogenesis; tumour; retinal disorder; age-related macular degeneration; diabetic retinopathy; rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
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100.0%; Pred. No. 0.011;
ive 0; Mismatches 0; Indels
100.0%; Score 62; DB 2; Length 118; 100.0%; Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lowman HB,
                               0; Mismatches
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                                                                                                                                                                  AAW70682 standard; peptide; 118 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US006604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00833504
97US-00908469
                                                                                                                                                                                                                             (first entry)
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Matches 10; Conservative
                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-568337/48
                                                               1 GYDFTHYGMN
                                                                                         26 GYDPTHYGMN
                 Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9845331-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1997;
                                                                                                                                                                                                                             27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-0CT-1998.
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                 AAW70682;
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                                                                                                                                      RESULT 10
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RESULT 11 AAB05900

cheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

Sequence 118 AA;

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Anti-VEGF antibody YO243-1 heavy chain variable domain.
The present sequence is the heavy chain variable domain of the F(ab)-12 antibody variant Y0238-3. F(ab)-12 is a humanised anti-vascular endothalial growth factor (VEGF) antibody. F(ab)-12 was the parent artibody used in the production of a large number of antibody variants containing randomised peptide inserts within the complementarity determining regions (CDRS). Phage display libraries were subjected to eight rounds of selection to isolate variants with an antigen binding affinity at least two-fold stronger than the binding affinity of parent antibody for the target VEGF antibody. The anti-VEGF antibody variants may be useful in diagnostic assays for detecting expression of VEGF in cells, tissue or serum. They may also be used in the prevention and treatment of neoplastic diseases such as breast cancer, lung cancer and arthritis, psoriaals, atherosclerosis, and diabetic and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody variants with higher binding affinity than native antibodies useful for diagnosis, prevention and treatment of neoplastic and non-neoplastic diseases comprises amino acid insertion in hypervariable
                                                                                                                                          Humanised; F(ab)-12; heavy chain variable domain; antibody variant; phage display; randomised library; cytostatic; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory; antiarteriosclerotic; vascular endothelial growth factor; def; breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis; psoriasis; atherosclerosis; diabetic retinopathy; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                          F(ab)-12 antibody variant Y0238-3 heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 62; DB 3; Length 118;
100.0%; Pred. No. 0.011;
ive 0; Mismatches 0; Indels
 AAB05900 standard; peptide; 118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 1B; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muller Y;
                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US027153
                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0108945P
                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYDFTHYGMN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYDFTHYGMN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen YM, Lowman HB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-387797/33
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                             WO200029584-A1
                                                                                                                                                                                                                                                                         Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                  16-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                               25-MAY-2000.
                                                                      17-0CT-2000
                                   AAB05900;
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AAB13382 standard; protein; 118 AA.

RESULT 12 AAB13382

ò 셤 (first entry)

21-NOV-2000

AAB13382;

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The present sequence is the heavy chain variable region of the affinity matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody voca-1. Humanised Febb-12 and affinity matured anti-VEGF) antibodis may be used to treat conditions characterised by undestrable excessive neovascularisation. Such conditions include tumours (especially solid neovascularisation. Such conditions include tumours (especially solid other retinopathies, retrolental fibroplasia, age-related macular degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias (including Grave's disease), corneal and other tissue transplantation, and chronic inflammation. Oedemas associated with malignancies, meig's syndrome, head trauma, and ascites associated with malignancies, meig's syndrome, lung inflammation, nephrotic syndrome, pericardial effusion and pleural effusion, may also be treated Monoclomal antibodies are generated in hybridoma cells and those with affinity for VEGF are identified by immunoprecipitation or by an in vitro binding assay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and chronic inflammation in a mammal, comprises administering a human vascular endothelial cell growth factor antagonist.
YO243-1; vascular endothelial cell growth factor; VEGF; antibody; antiinflammatory; cerebroprotective; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic; antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis; psoriasis; atherosclerosis; diabetes; retrolental fibroplasia; neovascular glaucoma; haemangloma; thyroid hyperplasia; Grave's disease; tissue transplantation; inflammation; oedema; trauma;
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                                                                                                                                                                                                                                  complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                               cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 14B; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                   26. .35
/label= CDR-H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              50. .66
/label= CDR-H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99. .112
/label= CDR-H3
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/label= CDR-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
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                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUN-2000
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AAB13385
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22-DEC-1998; **Jnidentified** 19-DEC-1999; 21-NOV-2000 29-JUN-2000 AAB13385 Region Region Region Region

Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and chronic inflammation in a mammal, comprises administering a human vascular endothelial cell growth factor antagonist. Y0317; vascular endothelial cell growth factor; VEGF; antibody; antilnflammatory; cerebroprotective; cytostatic; antinheumatic; antiarteritic; antisoriatic; antidabetic; antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis; psoriasis; atherosclerosis; diabetes; retrolental fibroplasia; tissue transplantation; inflammation; oedema; trauma; Grave's disease; complementarity determining region; CDR. Anti-VEGF antibody YO317 heavy chain variable domain. Location/Qualifiers Disclosure; Fig 14B; 60pp; English. AAB13385 standard; protein; 118 AA. 16. .35 |abel= CDR-H1 99. .112 /label= CDR-H3 CDR-H2 70. .79 /label= CDR-7 98US-00218481. 99WO-US029475 Van Bruggen N, Ferrara N; (first entry) 50. .66 /label= (GETH) GENENTECH INC WPI; 2000-442646/38. WO200037502-A2

The present sequence is the heavy chain variable region of the affinity matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody (YO17). Humanise Febb-12 and affinity matured anti-VEGF antibodies may be used to treat conditions characterised by undesirable excessive neovascularisation. Such conditions include tumours (especially solid comes), rheumatoid arthritis, psoriasis, atherosoflerosis, diabetes and coher retinopathies, retrolental fibroplasia, age-related macular degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias (including Grave's disease), corneal and other tissue transplantation, and chronic inflammation. Ocdemas associated with tumours, strokes and head trauma, and ascites associated with malignancies, meig's syndrome, lung inflammation, nephroite syndrome, pericadial effusion and pleural effusion and pleural effusion and pleural hybridoma cells and those with affinity for VEGF are identified by immunoprecipitation or by an in vitro binding assay

Sequence 118 AA;

Gaps ô 100.0%; Score 62; DB 3; Length 118; 100.0%; Pred. No. 0.011; ive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 10; Conservative

26 GYDFTHYGMN 35

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RESULT 14 AAB1338

Ź AAB13384 standard; protein; 118

AAB13384;

(first entry) 21-NOV-2000 Anti-VEGF antibody Y0313-1 heavy chain variable domain.

antiinflammatory; cerebroprotective; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic; antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis; psoriasis atherosclerossis; diabetes; retrolental fibroplasia; neovascular glaucoma; haemangioma; thyroid hyperplasia; drave's disease; tissue transplantation; inflammation; oedema; trauma; (0313-1; vascular endothelial cell growth factor; VEGF; antibody;

Unidentified

Location/Qualifiers 26. .35 /label= CDR-H1 Region Region

50. .66 /label= CDR-H2 70. .79 99. .112 /label= CDR-H3 /label= CDR-7 Region Region

WO200037502-A2

29-JUN-2000

99WO-US029475 09-DEC-1999; 98US-00218481 22-DEC-1998;

(GETH) GENENTECH INC

Van Bruggen N, Ferrara

ż

WPI; 2000-442646/38.

Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and chronic inflammation in a mammal, comprises administering a human vascular endothelial cell growth factor antagonist.

Disclosure, Fig 14B; 60pp; English.

The present sequence is the heavy chain variable region of the affinity matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody constructed anti-vascular endothelial cell growth factor (anti-VEGF) antibody voli3-1. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may be used to treat conditions characterised by undesirable excessive neovascularisation. Such conditions include tumours (especially solid ones), rheumatoid arthitis, psoriasis, atherosclerosis, diabetes and other retinopathies, retrolental fibroplasia, age-related macular degeneration, neovascular glaucoma, hasmangionas, thyroid hyperplasias of including Grave's disease), corneal and other tissue transplantation, and chronic inflammation. Ocembal and other tissue transplantation, and ascites associated with malignancies, meig's syndrome, head trauma, and ascites associated with malignancies, meig's syndrome, clusion, may also be treated. Monoclonal antibodies are generated in thybridoma cells and those with affinity for VEGF are identified by immunoprecipitation or by an in vitro binding assay

Sequence 118 AA;

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Query Match

100.0%; Score 62; DB 3; Length 118;

1 GYDFTHYGMN 10

Gaps

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Indels

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0; Mismatches

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10; Conservative
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to humanised anti-VEGF (vascular endothelial growth factor) antibodies or a variant of a parent anti-VEGF antibody, which binds human VEGF. The anti-VEGF antibodies are useful for inhibiting VEGF-induced angiogenesis in a mammal (particularly a human), particularly those having a tumour a retinal disorder e.g. intraocular neovascular disorders. The present sequence is an exemplary heavy chain variable domain of the humanised anti-VEGF antibody of the invention
                                                                                                                                                                                                                  Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF; vascular endothelial growth factor; angiogenesis inhibitor; tumour; retinal disorder; intraocular neovascular disorder; Y0313-1; heavy chain; variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New humanized anti-VEGF (vascular endothelial growth factor) antibodies or their variants, useful for inhibiting VEGF-induced angiogenesis in a mammal, particularly for treating tumor or retinal disorders.
            Gaps
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                                                                                                                                                                                              Humanised anti-VEGF Y0313-1 antibody variable heavy domain.
; Pred. No. 0.011;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wells JA, Presta LG, Lowman HB,
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                        ABP61255 standard; protein; 118 AA.
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/label= CDR-H2
70..79
/label= CDR-7
99..112
/label= CDR-H3
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100.0%;
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                                                                                                                                                                       (first entry)
 Best Local Similarity 100.
Matches 10; Conservative
                                   1 GYDFTHYGMN 10
                                                    WELLS J A.
PRESTA L G.
LOWMAN H B.
CHEN Y M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-517920/55.
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Best Local Similarity
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                                                                                                                                                                       20-SEP-2002
                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                Mus sp.
Synthetic.
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ABP61255
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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sw model protein search, using OM protein

April 25, 2006, 06:15:41; Search time 8.49057 Seconds (without alignments) 113.322 Million cell updates/sec Run on:

US-10-764-428-18 62 1 GYDFTHYGMN 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	lon	chain V r				chain V a	당	chain V r				chain V			chain V r		chain V r	>			chain V			chain V r	chain V r					
	Description	Ig heavy	Ig heavy	Ig heavy			Ig heavy		Ig heavy			L6 mAb heavy	Ig heavy	Ig heavy	Ig heavy	Ig heavy	Ig heavy	Ig heavy	Ig heavy	neavy	9010	heavy					מ	מ	ы	Ig heavy
	QI.	C24672	826326	D24672	S24764	S24765	826325	S19968	819965	819967	A53285	B42848	PH1404	833905	A49021	S46460	B36259	822552	PH1521	PH1519	835759	PH1489	PH1516	PH1488	A36194	B28572	B24754	A28572	PH1491	PH1490
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عد	Query Match	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4		77.4	77.4	74.2			•		74.2	74.2	74.2	72.6	72.6	71.0	67.7	67.7	67.7	67.7	67.7
	Score	48	48	4			48	48	48	48	48			48	46	46	46	46	46	46	46	46	45	45	44	42	42	42	42	42
	Result No.	1	7	m	4	ĸ	9	7	00	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

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ALIGNMENTS

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S	72
55	67
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RESULT 1

C24672

Lag heavy chain V region (VMU-1) - mouse (fragment)

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Accession: C24672

R; Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A; Reference number: A91022; MUID:86055722; PMID:2998759

A; Accession: C24672

A; Residues: 1-93 «WIN>
A; Residues: 1-93

ö Gaps ö Length 93; 1; Indels Query Match 77.4%; Score 48; DB 2; Best Local Similarity 80.0%; Pred. No. 0.18; Matches 8; Conservative 1; Mismatches

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S26326

Ig heavy chain V region - mouse (fragment)

Ig heavy chain V region - mouse (fragment)

C;Species Mus musculus (house mouse)

C;Species Mus musculus (house mouse)

C;Accession: 826326

R;Stark, 8.B.; Caton, A.J.

J; Exp. Med. 174, 613-624, 1991

A;Title: Antibodies that are specific for a single amino acid interchange in a protein e A;Reference number: \$26309; MUID:91341421; PMID:1908510

A;Molecule type: mRNA A;Residues: 1-99 <STA> A;Croserserseferences: UNIPARC:UF100001769AC; EMBL:X59174 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin

Gapa ö 77.4%; Score 48; DB 2; Length 99; 80.0%; Pred. No. 0.19; iive 1; Mismatches 1; Indels Query Match
Best Local Similarity 80.0
Matches 8; Conservative

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1 GYDFTHYGMN 10 ઠે 윱

GYTFTNYGMN 15

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A;Molecule type: DNA
A;Residues: 1-105 <KLA>
A;Cross-references: UNIPARC:UP1000011648E; EMBL:Z15001
A;Accession: S24773
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A;Residues: 1-105 <THO>
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A;Residues: 1-109 <STA>
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                                                                                                                                                                                                                                                                     A, Molecule type: DNA
          A; Accession: S24765
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Ig heavy chain V region (subgroup XI) - mouse (fragment)

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Date: 20-Feb-1995 #sequence revision 21-Nov-1998 #text_change 23-Jul-1999

C; Accession: S24764; S24777

R; Kiages, S.

submitted to the EMEL Data Library, August 1992

A; Reference number: S24764

A; Rocession: S24764

A; Rocession: S24774

A; Molecule type: DNA

A; Residues: 1-105 < KIA>

A; Rocession: S24772

A; Molecule type: DNA

A; Residues: 1-105 < KIA>

A; Rocession: S24776

A; Molecule type: DNA

A; Reference number: S24777

A; Molecule type: DNA

A; Residues: 1-105 < KIMO

A; Residues: 1-105 < KI
RESULT 3
D24672
Ig heavy chain V region (VGAM3-8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: D24672
EMBO J. 4, 2861-2867, 1985
A;Reference number: A91022; MUID:86055722; PMID:2998759
A;Accession: D24672
A;Molecule type: DNA
A;Residues: 1-101 <WIN>
A;Cossareferences: UNTPARC:UPIO000113758; GB:X03301; NID:G51757; PIDN:CAA27040.1; PID:G5Speriamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence revision 21-Nov-1998 #text_change 23-Jul-1999
C;Accession: 824765; 824773; $\overline{8}$24778
R;Klages, S.
B;Klages, C.
B;Klages, C.
B;Klages, S.
B;Klag
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80.0%; Pred. No. 0.2;
ive 1; Mismatches 1; Indels
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 80.0
Matches 8; Conservative
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Matches 8; Conservative
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C;Accession: S26325
R;Stark, S.E.; Caton, A.J.
Bxp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein el A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26325
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C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;5-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                A; Cross-references: UNIPARC: UP1000011648E; EMBL: Z15022; NID: 952619; PIDN: CAA78741.1; PID
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S19968
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004
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A;Molecule type: mRMP
A;Residues: 1-115 <#RI>
A;Residues: 1-115 <#RI>
A;Cross-references: UNIPROT:Q921A6; UNIPARC:UPI000017696A; EMBL:X65089
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C;Keywords: heterotetramer; immunoglobulin
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77.4%; Score 48; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 0.21;
Matches 8; Conservative 1; Mismatches 1; Indels
A,Cross-references: UNIPARC:UPI000011648E; EMBL:Z15013
R,Thomas, J.W.
submitted to the EMBL Data Library, August 1992
A,Reference number: $24776
A,Accession: $24778
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A, Cross-references: UNIPARC: UPI000017694C
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Ig heavy chain V region (M-T321) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Peb-1995 #sequence_revision 06-Peb-1995 #text_change 31-Dec-2004
C;Accession: S19965
R;Weissenhorn, W:; Riethmueller, G:; Weiss, E.M.; Rieber, B.P.
R;Weissenhorn, W:; Riethmueller, G:; Weiss, E.M.; Rieber, B.P.
A;Pescription: Structural characterization of CD4 mAb.
A;Reference number: S19965
A;Accession: S19965
A;Accession: S19965
A;Accession: S19965
A;Accession: UNIPROT:0921A6; UNIPARC:UPI0000176968; EMBL:X65088
C;Superfamily: immunoglobulin homology < IMM>
F;8-91/Domain: immunoglobulin homology < IMM>
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                                                                                                           77.4%; Score 48; DB 2;
80.0%; Pred. No. 0.22;
iive 1; Mismatches 1
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C;Keywords: heterotetramer; immunoglobulin P;10-93/Domain: immunoglobulin homology <IMM>
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Best Local Similarity
Matches 8; Conserv
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R;Sawada, J; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
Mol. Immunol. 28, 1063-1072, 1991
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary strucand their pH-reactivity profiles.
A;Reference number: A53285; MUID:92017897; PMID:1922102
                                                                                                                                                                                                                  A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA; protein
A;Cross-references: UNIPARC:UP1000011D0A7; GB:D12736; NID:g220595; PIDN:BAA02228.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBIP:63299)
A;Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBIP:63299)
C;Gyberfamily: immunoglobulin jammunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;15-99/Domain: immunoglobulin homology <IMM>
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C; Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C; Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
R; Pell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo
J; Biol. Chem. 267, 15552-1558, 1992
J; Biol. Chem. 267, 15552-1558, 1992
A; Title: Chimeric Lo anti-tumor antibody. Genomic construction, expression, and characte
A; Reference number: A42848; MUID:92348410; PMID:1639794
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A;Solatus: preliminary
A;Residues: 1-120 «FEL»
A;Cross-references: UNIPARC:UPI0000115333; GB:M90690; NID:g195065; PIDN:AAA38146.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBIP:109961)
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C;Species: Mus musculus (house mouse)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: FH404; PH1406
R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; T.J. Exp. Med. 176, 1209-1214, 1992
A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Reference number: PH1403; MUID:93018837; PMID:1402663
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Pred. No. 0.23;
1; Mismatches
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Pred. No. 0.23;
1; Mismatches
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80.0%;
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Best Local Similarity 80.v.
Rest Local Similarity
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A,Molecule type: DNA
A,Residues: 1-124 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <FE2>
C; Accession: A53285
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Search completed: April 25, 2006, 06:26:12 Job time : 8.49057 secs
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533905
Gig heavy chain precursor V region - synthetic
C; Date: 13-Jan-1995 #sequence_revision 30-Apr-1998 #text_change 20-Oct-2000
S; Date: 13-Signos #text_change 20-Oct-2000
S; Date: 13-Signos #text_change 20-Oct-2000
S; Date: 10-Signos #text_change 20-Oct-2000
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19 heavy chain V-XI region - African clawed frog (fragment)

C;Species: Xenopus laevis (African clawed frog)

C;Species: Xenopus laevis (African clawed frog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999

R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.

J. Exp. Med. 171, 1721-1737, 1990

A;Pitle: Eleven distinct V-H gene families and additional patterns of sequence variation

A;Pitle: Rieven distinct V-H gene families and additional patterns of sequence variation
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A, Status: preliminary; not compared with conceptual translation
A; Status: preliminary;
A; Molecule type: mRNA
A; Residues: 1-79 < HAI>
A; Residues: 1-79 < HAI>
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A;Accession: PH1406
A;Molecule type: DNA
A;Redidues: 115-121 <SH2>
A;Redidues: 115-121 <SH2>
A;Cross-references: UNIPARC:UPI000017694C
C;Genetics: cf.
A;Introns: 1cf.
C;Guperfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;35-118/Domain: immunoglobulin homology <IMM>
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80.0%; Pred. No. 0.24;
tive 1; Mismatches 1; Indels
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Pred. No. 0.34;
0; Mismatches 2; Indels
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45 GYTFTNYGMN 54
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RESULT 15 S46460 Ig heavy chain V region (YAC-10) - human

7 GYDFGSYGMN 16

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Ricook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Wint Nature Genet. 7, 162-168, 1994
Nature Genet. 7, 162-168, 1994
A;Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telome A;Reference number: S46460; MUID:95004581; PMID:7920635
A;Recession: S46460
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-98 <COO>
                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UP100001165DC; EMBL:227509; NID:9505445; PIDN:CAA81829.1; PIII C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
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80.0%; Pred. No. 0.43;
cive 0; Mismatches 2; Indels
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Matches 8; Conservative
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 25, 2006, 06:05:44 ; Search time 53.3962 Seconds (without alignments) 132.131 Million cell updates/sec Run on:

US-10-764-428-18 62 1 GYDFTHYGMN 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched: 2166443

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•			SOUTHWINE	
Result		Query				
No.	Score	Match	Match Length	08	ID	Description
-	46	74.2	125	7	Q6PILO HUMAN	
71	46	74.2	241	~	Q921A6 MOUSE	Q921a6 mus musculu
m	46	74.2	475	~	Q5PQS1_RAT	
4	43	69.4	176	N	OSOPUS_ENTHI	entamoeba
ß	43	69.4	237	7	Q50NY4_ENTHI	entamoeba
ø	43	69.4	238	N	Q50V47_ENTHI	entamoeba
7	43	69.4	260	7	Q50SP0_ENTHI	entamoeba
80	43	69.4	276	~	Q50T72 ENTHI	-
Ø,	43	69.4		N	QSONI1_ENTHI	_
10	43	69.4		7	Q840B9_9GAMM	ō
11	42	67.7	120	-	HV03 MOUSE	mu8
12	42	67.7	140	Н	HV02 MOUSE	
13	42	67.7	264	N	Q5KXS0_GEOKA	-
14	42	67.7	515	7	Q74LM7_LACJO	
15	42	67.7	562	~	Q70CA8_STRTR	
16	42	67.7	562	7	Q935T8_STRTR	
17	41	66.1	124	7	Q9NOW4_RABIT	
18	41	66.1	124	~	O9NOW6 RABIT	
19	41	66.1	162	~	Q6J192_9EURY	Q6ji92 uncultured
20	41	66.1	313	~	Q752R9 ASHGO	
21	41	66.1	447	~	QSCJA1_CRYHO	
22	41	66.1	449	N	Q5CXK4_CRYPV	-
23	41	66.1	454	7	Q82P16 STRAW	
24	41	66.1	853	~	Q7XL98_ORYSA	-
25	41	66.1	1417		Q4UIZ2_THEAN	-
56	41	66.1	1668		Q4UPD6 THEAN	_
27	41	66.1	1931	~	Q4UPL3_THEAN	-
28	41	66.1	2123		Q4UHHO THEAN	theileria
53	41	66.1	2364		Q4UEI6 THEAN	•
30	41	66.1	2732		Q4UJ64 THEAN	_
31	41	66.1	3096		Q4UCL8_THEAN	Q4ucl8 theileria a

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# ALIGNMENTS

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Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
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Eukaryota; Entamoebidae; Entamoeba.
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Interpro; IPR003599; IG.
Interpro; IPR03599; IG_C1.
Interpro; IPR03596; IG_WHC.
Interpro; IPR03596; IG_WHC.
Pfam; PR07654; C1-set; 2.
SWART; SM00409; IG; 3.
SWART; SM00406; IGC1; 3.
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D QFOPUS;
AC QSOPUS;
DT 13-SEP-2005 (TERMBLrel. 31,
DT 13-SEP-2005 (TERMBLrel. 31,
DT 13-SEP-2005 (TERMBLrel. 31,
DT 13-SEP-2005 (TERMBLrel. 31,
DT 078Names=357.00005;
ORVANAMES=357.00005
ORVANAMES=357.00005
OR ENKARYOCA; ENTAMOEDIAE;
OC BRAYOCA; ENTAMOEDIAE;
CO BRAYOCA; ENTAMOEDIAE;
CO BRAYOCA; ENTAMOEDIAE;
CO BRAYOCA; ENTAMOEDIAE;
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MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
Stark S.E., Caton A.J.;
Stark S.E., Caton A.J.;
"Antibodies that are specific for a single amino acid interchange in a protein epitope use structurally distinct variable regions.";
J. Exp. Med. 174.613.624(1991).
BMBL; U88067; AAB48044.1; -; mRNA.
PIR; $19967; $19967.
PIR; $19968; $19968.
PIR; $19968; $19968.
PIR; $19969; $19968.
                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2001 (TrEMBLrel. 26, Last annotation update)
Anti-CRA 79 single chain FV (Fragment).
Mus musculus (Mouse).
Bukaryota, Metzaoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Musmanalia, Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98170165; PubMed=9509426; Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D., Yi K.S., Suh P.G., Ryu S.H., Chung H.K.; Choring and characterization of coMse encoding VH and VL of a generation of anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and generation of a single-chain FV molecule (scFv).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                        DB 2; Length 125
                                                                         2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                  241 AA.
                        Score 46; DB 2
Pred. No. 2.5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                PRT;
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InterPro; IPR003596; Ig_v.
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                        74.2%;
80.0%;
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QSPQS1_
01-FEB-2005 (TEMBLrel. 29,
01-FEB-2005 (TEMBLrel. 29,
01-FEB-2005 (TEMBLrel. 29,
                                                                                                                                                                                                                                                                                                          Q921A6 MOUSE PRELIMINARY;
Q921A6;
Query Match
Best Local Similarity 80...
Best Local 8; Conservative
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                                                                                                                            1 GYDFTHYGMN 10
                                                                                                                                                                                45 GYSFTTYGMN 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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Name=Igha;
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SEQUENCE
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RESULT 2

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RESULT 3
Q5PQS1 RA
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DC Q5PQ
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MEDLINE-218825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-228825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-228825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MAISTORNER R.D., Colling F.S., Wagger L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
A stapleton M., Sares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,
A Nilalon D.K., Muzny D.W., Sodergren B.D., Dickson M.C.,
A Mitting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Beneration and initial analysis of more than 15,000 full-length human
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO87057; AAH87057.1; -; mRNA.
GO; GO:0003823; F:antigen binding; IEA.
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 475 AA; $2118 MW; EC61093E69A96708 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 9.9;
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PubMed=15729342; DOI=10.1038/nature03291;
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PubMed=15729342; DOI=10.1038/nature03291;

PubMed=15729342; DOI=10.1038/nature03291;

PubMed=15729342; DOI=10.1038/nature03291;

A medeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,

A medeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,

B. Hofer M., Burchhaus I., Willhoeft U., Bhattacharya A.,

Chillingworth T., Churcher C., Hance S., Harris B., Mitchead S.,

A gels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

Chillingworth T., Churcher C., Stroup S.B., Enbattacharya S.,

Guillen N., Gilchrist C., Stroup S.B., Bhattacharya S., Lohia A.,

Roster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,

R. Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,

Praser C.M., Hall N.;

R. The genome of the protist parasite Entamoeba histolytica.";

Nature 433:865-868(2005).
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A Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T., A Bub B., Pop M., Duchene M., Ackers J., Tannich B., Leippe M., Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A., Chilingworth T., Churcher C., Hance Z., Harris B., Harris D., A Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S., Quail M.A., Rabbinowitsch B., Norbertczak H., Price C., Wang Z., Guilen N., Glichrist C., Stroup S.E., Bhattacharya S., Lohla A., Roster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C., RI-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B., Praser C.M., Hall N.,

The genome of the protist parasite Entamoeba histolytica.";

"The genome of the protist parasite Entamoeba histolytica.";

"The genome of the protist parasite Stramoeba histolytica.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 2; Length 176;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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SEQUENCE 237 AA, 27296 MW; CCE644C6F61A51E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 176 AA; 20448 MW; 916FBEE8A5F67B8C CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.
EMBL: AAFB01000926; EAL43614.1; -; Genomic_DNA.
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ORFNames=407.t00002;
Entamoeba histolytica HM-1:IMSS.
Bukaryota; Entamoebidae; Entamoeba.
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Best Local Similarity 70.07
Best Local 7; Conservative
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QSONY4 ENTHI PRELIMINARY;
QSONY4;
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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REGUENCE 238 AA; 27499 MW; 4354BED1DA574954 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                   13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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EMBL; AAFB01000602; EAL45460.1; -; Genomic_DNA.
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Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=294381;
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ORFNames=253.t00018, 8.t00068;
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Q50SPO;
OSOV47 ENTHI PRELIMINARY;
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Q840B9;
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Best Local Similarity 70.0
Matches 7; Conservative
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RX PubMed=15729342; DOI=10.1038/nature03291;

RX Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,

RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,

RA Amedeo P., Roncaglia P., Berriman M., Tannich E., Leippe M.,

RA Hofer M., Bruchhaus I., Willhoeft U., Bhatracharya A.,

RA Ghillingworth T., Churcher C., Hance Z., Harris B., Harris D.,

RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

RA Guillen N.A., Rabbinowitsch E., Norbertczak H., Price C., Wang Z.,

RA Guillen N., Glichrist C., Stroup S.E., Bhatracharya S., Lohia A.,

RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,

RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,

RA Fraser C. M., Hall N.,

Raser C. M., Hall N.,

RA Fraser C. M., Hall N.,

RI "The genome of the protist parasite Entamoeba histolytica.";

RI "The sequence shown here is derived from an

CC EMBL/Genbank/DbBJ whole genome shotgun (WGS) entry which is
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              -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                  69.4%; Score 43; DB 2; Length 260; 70.0%; Pred. No. 19;
                                                                                                                                                                                                                                     2; Indels
                                                             EMBL; AAFB01000720; EAL44622.1; -; Genomic DNA.
EMBL; AAFB01000042; EAL51409.1; -; Genomic_DNA.
InterPro; IPR008262; Lipase_AS.
InterPro; IPR000379; Ser_estra.
PROSTTE; PS00120; LiPASE_SER; UNKNOWN_1.
Hydrolase; Hypothetical protein.
SEQUENCE 260 AA; 29344 MW; 5D5298790487EC84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Hypothetical protein.
SEQUENCE 276 AA; 31441 MW; 285F6277B5ED0942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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InterPro; IRRO003089; AB hydrolase.
InterPro; IPR000379; Ser estra.
InterPro; IPR000379; Ser estra.
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ORFNames=240.t00009;

Entamoeba histolytica HM-1:IMSS.

Bukaryota; Entamoebidae; Entamoeba.

NCBI_TaxID=294381;
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QSONI1 ENTHI
ID QSONI1 ENTHI PRELIMINARY;
AC QSONI1;
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Best Local Similarity 70.0.
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Nature 433:865-868(2005).
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Matches 7; Conservative
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                                                    preliminary data.
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STRAIN-HW-1:IMS;

X PubMed-a:1723942; DoI=10.1038/nature03291;

X PubMed-a:1723942; DoI=10.1038/nature03291;

Amedeo P., Anderson I., Davies R., Alsmark U.C., Samuelson J.,

Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,

Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,

And P., Pop M., Duchene M., Ackers J., Tannich B., Leippe M.,

Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,

Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,

Angels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

Angels K., Rabbinowitsch B., Norbertczak H., Price C., Wang Z.,

Guill M.A., Rabbinowitsch B., Norbertczak H., Price C., Wang Z.,

Angels K., Rabbinowitsch B., Norbertczak H., Price C., Wang Z.,

Angels K., Rabbinowitsch B., Norbertczak H., Barrell B.,

Fraser C.M., Hall N.,

The genome of the protist parasite Entamoeba histolytica.";

Nature 433:865-868(2005).

C. CAUTION: The sequence shown here is derived from an EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
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Biochem. J. 371:1027-1043(2003).

Biochem. J. 371:1027-1043(2003).

GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; I GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0006809; P:mannan metabolism; IEA.

InterPro; IPR002883; Dockerin_CBD_5.
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MEDLINE-22588103; PubMed=12523937; DOI=10.1042/BJ20021860;
Hogg D., Pell G., Dupree P., Goubet F., Martin-Orue S.M., Armand
Gilbert H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cellvibrio japonicus.
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadacese, Cellvibrio.
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EMBL, AAFBOL001078; EAL43151.1; -; Genomic_DNA.

InterPro; IPR003089; AB hydrolase.

InterPro; IPR007039; LRE Tp.

InterPro; IPR000379; Ser_estrs.

PRINTS; PR0011; ABHYDROLASE.

Hydrolase; Hypothetical protein.

SEQUENCE 348 AA; 39832 MW; 6482585020803E85 CRC64;
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=437.100002;
Entamoeah histolytica HM-1:IMSS.
Eukaryota, Entamoebidae; Entamoeba.
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01-070-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Endo-bl,4-mannanase 26B.
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1 GYDFTHYGMN 10
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P01746;
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Parhami-Seren B., Viswanathan M., Strong R.K., Margolies M.N.;
Parhami-Seren Soft Margolies of fight-affinity preazophenylarsonate-specific antibodies generated by alanine scanning of heavy chain complementarity-determining region 2.";
J. Immunol. 167:5129-5135(2001).
-I. MISCELLANEOUS: From analysis of the sizes of several other differentiated genes that hybridize to this one, the authors conclude that all of these V regions have rearranged to the same J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
MEDLINE-83131846; PubMed=6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marshak-Rothstein A., and antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";

Bur. J. Immunol. 12:1023-1032(1982).
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                          69.4%; Score 43; DB 2; Length 486; 77.8%; Pred. No. 36; 1; Msmatches 1; Indels ive
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                                                                                                486 AA; 53233 MW; 0494751306D5DD70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SW00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
3D-structure; Hybridoma; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
13-SBF-2005 (Rel. 48, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                              120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1JFQ; X-ray; H=1-120.
Ensembl; ENSMUSG00000021155; Mus musculus.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig-like.
    InterPro; IPR000805; Glyco_hydro_26.
Pfam; PP02013; CBM 10; 1.
Pfam; PP02156; Glyco_hydro_26; 1.
PRINTS; PR00739; GLHYDRLASE26.
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                             Query Match 69.4
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                          198 GYDFMNYGM 206
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Best Local Similarity
Matches 7; Conservat
                                                                                                                                                                                                                                           1 GYDFTHYGM 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A94264; HVMSG7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                            HV03 MOUSE
P01747;
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SEQUENCE
                                                                                                     SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatic and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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01-PEB-2005 (TrEMBLrel. 29, Last sequence update)
01-PEB-2005 (TrEMBLrel. 29, Last annotation update)
80-PEB-2005 (TrEMBLrel. 29, Last annotation update)
80-Vallation specific Nacetylmuramoyl-L-alanine amidase (Spore cortex-lytic enzyme) (RC 3.5.1.28).
OrderedLocusNames=GK2231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J00493; AAA38128.1; -; mRNA.
HSSP; P01747; 1JFQ.
SMR; P01746; 20-140.
InterPro; IPR00710; Ig-like.
InterPro; IPR03596; Ig_v.
SMRAT; SM0406; IGv. 1.
PROSITE; PSS0815; IG LIKE; 1.
PROSITE; PSS0815; IG LIKE; 1.
Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Capra J.D.;
"Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.";
Science 216:309-311(1982).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geobacillus kaustophilus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1; Length 140;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region 93G7 Ig-like.
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                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region 93G7 precursor. Mus musculus (Mouse).
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                                                                                                                                                                                                                             PRT;
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70.0%;
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OSKOS GEOKA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 70.0
                                                                                                                                                                                                                             STANDARD;
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GYTPTSYGIN 34
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102 GYHYTHFGSN 111
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                                                                                                         RESULT 15
Q70CA8_STRTR
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                          STRAINTHARAS;

STRAINTHARAS;

Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,

Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,

Matsui S., Uchiyama I.;

"Thermoadaptation trait revealed by the genome sequence of
thermophilic Geobacillus kaustophilus.";

II Nucleic Acids Res. 32:6292-6303[2004].

EMBL; BAD00043; BAD76316.1; -; Genomic_DNA.

GO; GO:0005618; C:cell wall; ERA.

GO; GO:00057618; F:hydrolase activity; IEA.

RO; GO:000847; F:hydrolase activity; IEA.

RO; GO:000947; P:peptidoglycan metabolism; IEA.

RO; GO:000947; P:peptidoglycan metabolism; IEA.

RO; GO:000947; P:peptidoglycan metabolism; IEA.

RO; GO:000946; Hydrolase delbydro.

RICEPPO; IPR011105; Ble Bydro.

Refam; PF01411; PG_binding_1; 1.

Refam; PF01411; PG_binding_1; 1.

Complete proteome Hydrolase.

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PubMed=14983040; DOI=10.1073/pnas.0307327101;

Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,

Pridmore A.C., Zewhlen M.-C., Rouvet M., Altermann B., Barrangou R.,

Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;

"The genome sequence of the probiotic intestinal bacterium for intestinal fo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.7%; Score 42; DB 2; Length 515; Best Local Similarity 60.0%; Pred. No. 57; Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactobacillus johnsonii.
Bacteria, Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00953; GLYCOSYL HYDROL F25; UNKNOWN 1.
Complete proteome; Hypothetical protein.
SEQUENCE 515 AA; 55968 MW; 0D08FB65591ACD04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 AA; 29204 MW; 70ED5F2B46051811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q74LM7_LACJO PRELIMINARY; PRT; 515 AA.

Q774LM7;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Mycythetical protein.
OrderedLocusNames=LJ0156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] STRAIN=NCC 533;
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Best Local Similarity 87.5'
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Pavlovic G., Burns V., Gintz B., Decaris B., Guedon G.;

"Byolvution of genomic islands by deletion and tandem accretion by site-specific recombination: ICESt1-related elements from site-specific recombination: ICESt1-related elements from Microbiology 50:759-774 (2004).

EMBL, AJS86568; CAES2361.1; -; Genomic_DNA.

PERS. PROSESS FERK SPOILE: 1.

PROSITE; PSS0901; FTSK, 1.
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                                                                                                                                     Streptococcus thermophilus.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                 Last sequence update)
Last annotation update)
  562 AA
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Job time : 56.3962 secs
  PRT;
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Q70CA8 STRTR PRELIMINARY;
Q70CA8;
O5-UUL-2004 (TrEMBLrel. 27, C:
05-UUL-2004 (TrEMBLrel. 27, Li
05-UUL-2004 (TrEMBLrel. 27, Li
Putative transfer protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 77.8 hes 7; Conservative
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294 GKNFTHYGM 302
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                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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GenCore version 5.1.7
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- protein search, using sw model OM protein

April 25, 2006, 06:25:05; Search time 13.4906 Seconds (without alignments) 61.284 Million cell updates/sec Run on:

US-10-764-428-18 62 1 GYDFTHYGMN 10 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

572060 segs, 82675679 residues Searched: 572060 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

					SUMMARIES	
Result No.	Score	Query Match	Length	DB	αı	Description
	62	100.0	10	7	US-08-908-469-86	Sequence 86, Appl
~	62	100.0	10	~	US-08-908-469-128	128
m	62	100.0	118	~	US-09-440-781-97	97,
4	62	100.0	118	7	US-08-908-469-112	Sequence 112, App
Ŋ	62	100.0	118	7	US-08-908-469-116	116,
•	62	100.0	118	~	US-08-908-469-118	
7	62	100.0	121	N	US-09-440-781-99	66
60	28	93.5	10	~	US-08-908-469-88	88
0	58	93.5	10	~	US-08-908-469-90	90,
10	55	88.7	10	~	US-08-908-469-89	89,
11	54	87.1	10	~	US-08-908-469-91	Sequence 91, Appl
12	52	83.9	10	~	US-08-908-469-87	87,
13	51	82.3	10	N	US-09-440-781-19	19,
14	4	79.0	160	~	US-09-318-786-35	35
15	48	77.4	10	~	US-09-440-781-20	50,
16	48	77.4	10	7	US-08-908-469-1	Sequence 1, Appli
17	48	77.4	92	~	US-08-783-853A-84	
18	48	77.4	92	~	US-09-344-050-84	84,
19	48	77.4	112	~	US-08-783-853A-20	20,
50	48	77.4		7	US-09-344-050-20	20,
21	48	77.4	118	-	US-08-425-336-124	
22	48	77.4	118	Н	US-08-425-336-126	126,
23	48	77.4	118	-	US-08-488-113B-124	124,
24	48	77.4		-	US-08-488-113B-126	126,
25	48	77.4	118	Н	US-08-477-484B-124	Sequence 124, App
56	48	77.4		Н	US-08-477-484B-126	126,
27	48	77.4	118	-	US-08-107-669D-28	Sequence 28, Appl

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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels

Sequence 29, Appl Sequence 66, Appl Sequence 67, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 67, Appl Sequence 67, Appl Sequence 124, Appl Sequence 28, Appl Sequence 28, Appl Sequence 29, Appl Sequence 29, Appl Sequence 28, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 214, Ap		•
28 48 77.4 118 1 US-08-107-669D-29 Se 29 48 77.4 118 1 US-08-107-669D-66 Se 31 48 77.4 118 1 US-08-107-669D-67 Se 31 48 77.4 118 1 US-08-472-788A-28 Se 33 48 77.4 118 1 US-08-472-788A-89 Se 34 48 77.4 118 1 US-08-472-788A-89 Se 31 48 77.4 118 1 US-08-472-788A-89 Se 31 48 77.4 118 1 US-08-477-531B-29 Se 31 48 77.4 118 1 US-08-477-531B-67 Se 31 48 77.4 118 1 US-08-477-531B-67 Se 41 48 77.4 118 1 US-08-477-531B-67 Se 41 48 77.4 118 1 US-08-477-531B-67 Se 41 48 77.4 118 1 US-08-646-360-124 Se 41 48 77.4 118 1 US-08-646-360-124 Se 41 48 77.4 118 1 US-08-082-842A-29 Se 42 44 48 77.4 118 1 US-08-082-842A-29 Se 44 48 77.4 118 1 US-08-082-842A-89 Se 44 48 77.4 118 1 US-08-082-842A-89 Se 44 48 77.4 118 1 US-08-082-842A-89 Se 45 77.4 118 2 US-08-939-765-124 Se	ALIGNMENTS  ALIGNMENTS  US-08-908-469-86  1 Sequence 86, Application US/08908469  1 Patent No. 688487108:  APPLICANT: Baca, Manuel  APPLICANT: USA  CITY: South San Francisco  STREET: California  COUNTRY: USA  COUNTRY: USA  COUNTRY: USA  COUNTRY: USA  COUNTRY: USA  CONTRY: USA  CONTRY: USA  CONTRY: USA  CONTRY: 21 MAY-2001  CLASSIFICATION NUMBER: US/08/908,469  FILING DATE: 21 MAY-2001  CLASSIFICATION NUMBER: US/08/908,469  FILING DATE: 21 MAY-2001  CLASSIFICATION NUMBER: UNMONENTER PROPERTION: AUTHOWN-  PRIOR APPLICATION NUMBER: UNMONENTER PROPERTION: AUTHOWN-  TELECOMMUNICATION INFORMATION:  ATTORNEY/AGENT INFORMATION:  TELECHONER COUNTS ESQ ID NO: 86:  SEQUENCE CHARACTERISTICS:  LENGTH: 10 amino acids  TYPE: Amino Acid  TYPE: Amino Acid	

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ORGANISM: artificial sequence
FEATURE:
LOCATION: 1-118
COTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 62; DB 2; Length 118; 100.0%; Pred. No. 0.0055; Pred. 0, Mismatches 0; Indels
                                                                                                                                                            100.0%; Score 62; DB 2; Length 118, 100.0%; Pred. No. 0.0055;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITTES SOUTH SAN FRANCISCO
STATE: California
COUNTY: South San Francisco
COUNTY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIPICATION NUMBER: 08/839.504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NEWSISTRATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NEWSISTRATION NUMBER: 44,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P1093P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 112, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
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INFORMATION FOR SEQ 1D NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1 DNA Way
                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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US-08-908-469-112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 11M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                      APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/833,504
ELLING DATE: 07-APR-1997
ATTONNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 128:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yvonne Man-yee Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 97
                                                                                                                                            Sequence 128, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-440-781-97
; Sequence 97, Application US/09440781
; Setten No. 6632926
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
GYDFTHYGMN 10
                   GYDFTHYGMN 10
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                                                                                                                           US-08-908-469-128
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OTHER INFORMATION: humanized antibody heavy chain variable domain
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    COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION SAR-1997
APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTATION NUMBER: 44,637
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 650/225-8674
TELEPRAK: 650/225-8674
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 62; DB 2;
100.0%; Pred. No. 0.0056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 99, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: YVONNE Man-yee Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
PILE REFERENCE: P1465R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 118: US-08-908-469-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-08-469-88
Sequence 88, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 118 amino acida TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: artificial sequence
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                           COMPUTER: CALIFORNIA
COMPUTER: CALIFORNIA
ZIP: 94080
ZIP: 94080
COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: L-MAY-2001
CLASSIFICATION: cUMCHOMN->
PRIOR APPLICATION: cUMCHOMN->
PRIOR APPLICATION: CUMCHOMN->
PRIOR APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INPORMATION:
RECISTRATION NUMBER: P1093P1
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAX: 650/952-9881
INPORMATION POR SEQ ID NO: 116:
SEQUENCE CHARACTERESTICS:
TEMPORMATION POR SEQ ID NO: 116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 118, Application US/08908469
; Patent No. 6884879
; GENERAL INPORMATION:
GENERAL INPORMATION:
MAINER ADDITION:
Presta, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
COMEN YVONDE M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
      US-08-908-469-116
; Sequence 116. Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Presta, Leonard G.
; Lownan, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 116: US-08-908-469-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 118 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
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Best Local Similarity
Matches 10; Conserv?
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Score 58; DB 2; Length 10;
Pred. No. 0.0019;
1; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 89, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 131
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION AND ATA:
APPLICATION NUMBER: 08/833,504
FILING DATE: 07-ARR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cul, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-861
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cul. Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 90:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GYDFTHYGMN 10
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90.0%; Pred. No. 0.0019;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: READABLE FORM:
COMPUTER: DAY COMPUTED:
COMPUTER: DAY COMPUTED:
COMPUTER: WinPatin (Genentech)
CURRENT APPLICATION DATA:
PRILOR DATE: 21-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 44,637
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/952-9674
TELEFAX: 650/952-9674
TELEFAX: 650/952-9674
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-08-908-469-90
i Sequence 90, Application US/08908469
i Patent No. 6884879
i GENERAL INPORMATION:
i GENERAL INPORMATION:
i Harry B.
TITLE OF INVENTION: APTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSES: Genertech, Inc.
STRET: 1 DNA WAY
CITY: South San Francisco
STRETE: 1 DNA WAY
CITY: South San Francisco
STRETE: 1 DNA WAY
CITY: South San Francisco
STRETE: 1 DNA WAY
ZIP: 94080
NRUTER FFF
                             Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-08-908-469-88
                                                                                                                                    ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
           Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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Best Local Similarity
Matches 9; Conserva
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Score 51; DB 2; Length 10;
Pred. No. 0.026;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/908,469 FILING DATE: 21-May-2001 CLASSIPICATION NUMBER: 08/833,504 FILING DATE: 07-ARY-1997 ATTORNEY/AGENT INFORMATION: NUMBER: 08/833,504 RILING DATE: 07-ARY-1997 ATTORNEY/AGENT INFORMATION: NAMME: Cui, Steven X. REGISTRATION NUMBER: 44,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 2;
Pred. No. 0.018;
1; Mismatches
                                          Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/09440781
Sequence 19, Parent No. 6632926
GENERAL INFORMATION:
APPLICANT: Youne Man-yee Chen et al.
TILLE OF INVENTION: ANTIBODY VARIANTS
FILE REPERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 19
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P1093P1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: artificial LOCATION: 1-10 ; OCHER INFORMATION: variant CDR sequence US-09-440-781-19
                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                      CITY: South San Francisco
STATE: California
COUNTRY: USA
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.3%;
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80.0%;
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Best Local Similarity 80.v
Est.co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.9
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYEPQHYGMN 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-908-469-87
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Pred. No. 0.0084;
2; Mismatches 0; Indels
                                                            Score 55; DB 2; Length 10; Pred. No. 0.0058;
                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 11M PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,504
FILING DATE: 07-AR-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1
TELEPHONE: 650/225-8674
TELEPHONE: 650/225-8674
TELEPHONE: 650/225-8674
TELEPAX: 650/25-8674
TELEPAX: 650/952-981
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Linear SEQ ID NO: 91: US-08-908-469-91
      SEQUENCE DESCRIPTION: SEQ ID NO: 89:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 87, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
                                                                                                                                                                                                                                 RESULT 11
US-08-908-469-91
; Sequence 91, Application US/08908469
; Patent No. 6884879
; Patent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.1%;
80.0%;
                                                              88.7%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                     Best Local Similarity 90.0
Matches 9; Conservative
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1 GYEPSHYGMN 10
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US-08-908-469-87
                ;
US-08-908-469-89
                                                                     Query Match
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                                                                                                             US-05-318-786-35

Sequence 35, Application US/09318786

Patent No. 6472147

GENERAL INFORMATION:

APPLICANT: Janda, Kim D

APPLICANT: Wireching, Peter

APPLICANT: Wireching, Peter

APPLICANT: Lerner, Richard A

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: PILAMENTOUS PHAGE USING pvII AND DIX, COMPOSITIONS,

TITLE OF INVENTION: PILAMENTOUS PHAGE USING pvII AND DIX, COMPOSITIONS,

TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES

FILE REFERENCE: TSR0305S

CURRENT FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 39

SOUTHARE: Patentin Ver. 2.1

SEQ ID NO 35

LENTH: 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: fusion OTHER INFORMATION: polypeptide US-09-318-786-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
79.0%; Score 49; DB 2; Length 160;
Best Local Similarity 80.0%; Pred. No. 0.97;
Matches 8; Conservative 1; Mismatches 1; Indels
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77.4%; Score 48; DB 2; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.079;
Matches 7; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-003-440-781-20

Sequence 20, Application US/09440781

PAtent No. 6813296

SERERAL INFORMATION:

APPLICANT: Yvonne Man-yee Chen et al.

TITLE OF INVENTION: ANTIBODY VARIANTS

FILE REFERENCE: P1469R1

CURRENT APPLICATION NUMBER: US/09/440,781

CURRENT FILING DATE: 1999-11-16

NUMBER OF SEQ ID NOS: 99

SEQ ID NO 20

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 1-10
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: April 25, 2006, 06:28:40 , Job time : 13.4906 Becs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
               1 GYDFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GYDFTHYGMN 10
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1 GYDYTNYGIN 10
GYDFTHYGMN 10
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Sequence

56, Appl 136, App 140, App 140, App 11, Appl 11, Appl 11, Appl 11, Appl 127, App 127, App 127, Appl 127, A

Sequence Seq

US-10-723-434-56 US-10-779-392-136 US-10-379-392-136 US-10-379-392-148 US-10-379-392-148 US-10-379-392-148 US-10-697-995-9 US-10-697-995-9 US-10-764-428-7 US-10-764-428-7 US-10-773-434-127 US-10-773-434-127

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US-09-056-160B-88 US-09-056-160B-90 US-10-234-671-88 US-10-234-671-90

ALIGNMENTS

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           April 25, 2006, 06:58:17 ; Search time 43.5849 Seconds (without alignments) 95.866 Million cell updates/sec
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US-10-974-591-86
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US-10-234-671-110
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Gapop 10.0 , Gapext 0.5
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1B0D1ES floppy 60B	sections RF. Application US/09056160B		
Acca, Manuel Wells, James A. Prestat, Leonard G. Cowman, Henry B. Chen, Yvonne M. SWITCN: ANTI-VEGF ANTIBODIES Genentech, Inc. DADRESS: Genentech, Inc. DAR Way Chents and Francisco lifornia USA OBLE FORM: ES 3.5 inch, 1.44 Mb floppy disk IEM PC compatible SWITCH PC COMPATION: AN WINDER: US/09/056,160B N UNDER: 06-Apr-1998 TION: 424 ATTON: 424 ATTO	Sequence of, Application of, Control of Cont		
TESTA, JAMEB A.  JOWNAN, HENRY B.  JOHN YOUNG M.  THENY YOUNG M.  THENY SANTIBODIES  JUENCES: 131  THENDERSS:  GENERALCH, INC.  DARLE FORM:  B. 3.5 inch, 1.44 Mb floppy disk  ILIORATION DATA:  N. NUMBER: US/09/056,160B  TION: 424  ATTON DATA:  N. NUMBER: 60/054,856  E. 06-AUG-1997  TI TRORAMATION:  ATTON INFORMATION:  ATTON OF 86:  RACTERISTICS:  O amino acids  Innear	Manuel		
Cowman, Henry B.  Chen, Yvonne M.  STATION: ANTI-VEGF ANTIBODIES  JUENCES: 131  SA ADDRESS:  GADRESS:  GADRESS:  ALL San Francisco  Lifornia  DAR Way  DABLE FORM:  B. 3.5 inch, 1.44 Mb floppy disk  IBM PC compatible  SYSTEM: PC-DOS/MS-DOS  WINDER: US/O9/056,160B  N NUMBER: US/O9/056,160B  N NUMBER: US/O9/056,160B  TION: 424  ATTON DATA:  N NUMBER: 28,616  DOCKET NU	Presta, Leonard		
Chen, Yvonne M.  SWINGS: 131  DERNORS: 131  SADDRESS: Genentech, Inc. DNA Way  DNA Way  DABLE FORM: SE: 3.5 inch, 1.44 Mb floppy disk IEM PC compatible SYSTEM: PC-DOS/MS-DOS WINDER: US/09/056,160B  N WUMBER: US/09/056,160B  N WUMBER: US/09/056,160B  N WUMBER: 60/054,856  N UNDER: 28,616  NUMBER: 28,616  NUMBER: 28,616  DOCKET NUMBER: 28,616	Lowman,		
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Libernia Lifernia Lifernia Lish DABLE FORM:  Example To Compatible SYSTEM:  PC-DOS/MS-DOS WINDRAIN (Genentech) ICATION DATA:  N NUMBER:  Example To Compatible N NUMBER:  N NON NUMBER:  N			
11fornia  USA  OBLE FORM:  DALE FORM:  18 3.5 inch, 1.44 Mb floppy disk  IEM PC compatible  SYSTEM: PC-DOS/MS-DOS  WINDER: PC-DOS/MS-DOS  WINDER: US/09/056,160B  B: 06-Apr-1998  R: 06-Apr-1998  R: 06-Apr-1998  R: 06-Apr-1998  WINDER: 60/054,856  N: UMBER: 60/054,856  N: UMBER: 28,616  DOCKET NUMBER: 28,616  DOCKET NUMBE			
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Dable FORM:  2. 3.5 inch, 1.44 Mb floppy disk IBM PC compatible SYSTEM: PC-DoS/MS-DOS Winbatin (Genentech) ICATION DATA: N WUMBER: US/09/056,160B RION: 424 ATTON DATA: N WUMBER: 60/054,856 E: 06-AUG-1997 NT INFORMATION: ATTON INFORMATION: AN UMBER: 28,616 DOCKET WUMBER: 91093R2 ATTON INFORMATION: 650/225-1896 G50/225-1896 G50/225-1896 G50/225-1896 G50/225-1896 G50/225-1896 DOCKET WUMBER: 28,616 DOCKET WUMBER: 28,61			
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8: 3.5 inch, 1.44 Mb iloppy disk SYSTEM: PC compatible SYSTEM: PC-DOS/MS-DOS WinPatin (Genentech) ICATION DATA: WINDER: US/09/056,160B R: 06-Apr-1998 R: 06-Apr-1998 R: 06-Apr-1998 R: 06-Aug-1997 RION: 424 ATION DATA: WINDER: 60/054,856 R: 06-Aug-1997 R: NUMBER: 28,616 B: 06-Aug-1997 R: NUMBER: 28,616 B: 06-Aug-1997 R: NUMBER: 28,616 B: 00 NUMBER: 191093R2 ATION INFORMATION: 650/25-1896 R: SEQ ID NO: 86: RACTERISTICS: 0 amino acids no Acid Linear Linear	COMPUTER READABLE FORM:		
IBM PC compatible SYSTEM: PC-DoS/MS-DOS Winbatin (Genentech) ICATION DATA: N VOMBER: US/09/056,160B RION: 424 ATTON: 424 ATTON DATA: NT INFORMATION: R: 06-AUG-1997 NT INFORMATION: AN UMBER: 28,616 DOCKET NUMBER: 28,616 DOCKET NUMBER: 28,616 NN NUMBER: 28,616 ATTON INFORMATION: 650/225-1896 RSGO ID NO: 86: RACTERISTICS: O amino acids IOO.0%; SCOTE 62; DB 3;	MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk		
SYSTEM: PC-DS/RS-DS WINDER: VC-DS/RS-DS N WUMBER: US/09/056,160B N WUMBER: US/09/056,160B TION: 424 ATTON DATA: ATTON DATA: ATTON DATA: RY INFORMATION: AN UMBER: 28,616 DOCKET NUMBER: 28,616 DOCKET NUMBER: P1093R2 ATTON INFORMATION: 650/252-1896 FSCO/252-1896 N SECOID NO: 86: RACTERISTICS: O amino acids INORAL SCOFE 62; DB 3;	COMPUTER: IBM PC compatible		
MUMBER: US/09/056,160B B: 06-Apr-1998 RITON: 424 ATION: 424 ATION DATA: N UNMBER: 60/054,856 RE: 06-AdG-1997 ATION TORNATION: ANY Janet E. DOCKET NUMBER: 28,616 DOCKET NUMBER: 28,616 ATION INPORMATION: ATION INPORMATION: 650/252-1896 650/252-1896 ATION: 86: RACTERISTICS: 0 amino acids 100.0%; Score 62; DB 3;			
N NUMBER: US/09/056,160B  8: 06-Apr-1998  AITON: 424  ATTON 424  ATTON DATA:  N NUMBER: 60/054,856  E: 06-AUG-1997  RY INFORMATION:  AK, Janet E.  ON NUMBER: 28,616  DOCKET NUMBER: P1093R2  ATTON INFORMATION:  650/252-9881  ATTON INFORMATION: 650/252-9881  FRACTERISTICS: 0 amino acids no Acid Linear  100.0%; Score 62; DB 3;	CHRRNT APPLICATION DATA:		
E: 06-Apr-1998 TION: 424 ATION: 424 ATION DATA: ATION DATA: NUMBER: 60/054,856 B: 06-AUG-1997 NT INFORMATION: AND NUMBER: 28,616 DOCKET NUMBER: 19,03R2 ATION INFORMATION: 650/225-1896 650/225-1896 650/225-1896 650/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150/225-1896 150	APPLICATION NUMBER: US/09/056,160B		
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ATION DATA:  N NUMBER: 60/054,856  N NUMBER: 60-AUG-1997  NT INFORMATION:  AX, Janet B.  DOCKET NUMBER: 28,616  DOCKET NUMBER: P1093R2  ATION INFORMATION: 650/252-1896 650/252-1896 650/252-9881  R SEQ ID NO: 86: RACTERISTICS: 0 amino acids no Acid Linear  100.0%: Score 62; DB 3;	CLASSIFICATION: 424		
N NUMBER: 60/054,856 E: 06-AUG-1997 NT INFORMATION: ak, Janet E. ON NUMBER: 28,616 DOCKET NUMBER: P1093R2 ATION INFORMATION: 650/252-1896 650/252-1896 650/252-1896 no AEG IN ON: 86: RACTERISTICS: 0 amino acids no Acid Linear 100.0%; Score 62; DB 3;	PRIOR APPLICATION DATA:		
E: 06-AUG-1997 NT INFORMATION: ANY JANEER: 28,616 DOCKET NUMBER: 28,616 E50/225-1896 E50/952-9881 R SEQ IN NO: 86: RACTERISTICS: 0 amino acids no Acid Linear 100.0%; Score 62; DB 3;	APPLICATION NUMBER: 60/054,856		
NT INFORMATION: ak, Janet E. ak, Janet E. bockst NUMBER: 28,616 bockst NUMBER: P1093R2 ATION INFORMATION: 650/225-1896 650/225-9881 R SEQ ID NO: 86: RACTERISTICS: 0 amino acids no Acid Linear 100.0%; Score 62; DB 3;	FILING DATE: 06-AUG-1997		
ak, Janet B. ON NUMBER: 28,616 ON NUMBER: P1093R2 ATION INFORMATION: 650/225-1896 650/225-1896 650/525-9891 R SEQ ID NO: 86: RACTERISTICS: 0 amino acids no Acid Linear 100.0%; Score 62; DB 3;	ATTORNEY/AGENT INFORMATION:		
ON NUMBER: 28,616 DOCKET NUMBER: 29,616 ATION INFORMATION: 650/252-881 650/252-9881 650/252-9881 650/252-9881 650/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881 670/252-9881	NAME: Hasak, Janet E.		
DOCKET NUMBER: P1093R2 ATION INFORMATION: 650/225-1896 650/52-9881 R SEQ ID NO: 86: RACTERISTICS: 0 amino acids no Acid Linear 100.0%; Score 62; DB 3;	Ψ		
ATION INPORMATION: 650/225-1896 650/952-9881 R SEQ ID NO: 86: RACTERISTICS: 0 amino acids Linear 100.0%; Score 62; DB 3;	REFERENCE/DOCKET NUMBER: P1093R2		
650/225-1896 650/952-9881 8 SEQ ID NO: 86: RACTERISTICS: 0 amino acids no Acid Linear 100.0%; Score 62; DB 3;	TELECOMMUNICATION INFORMATION:		
650/952-9881 RACTERISTICS: 0 amino acids no Acid Linear 100.0%; Score 62; DB 3;	TELEPHONE: 650/225-1896		
R SEQ ID NO: 86: RACTERISTICS: O amino acids Linear  100.0%; Score 62; DB 3;			
RACTERISTICS: 0 amino acids Linear 100.0%; Score 62; DB 3;			
O amino acids no Acid Linear 100.0%; Score 62; DB 3;	SEQUENCE CHARACTERISTICS:		
no Acid Linear 100.0%; Score 62; DB 3;	: 10 amino		
Linear 100.0%; Score 62; DB 3;			
100.0%; Score 62; DB 3;			
100.0%; Score 62; DB 3;	09-056-160B-86		
	n 100.0%; Score 62; DB 3;	10;	
nilarity 100.0%; Pr	Similarity 100.0%; Pred. No. 0.0016;		
TO DESCRIPTION OF THE PROPERTY	Matches 10; Conservative 0; Mismatches 0; inde-		
TO: COURSEIVACIAVE O; MISSINGACCIAS O; INC.			

1 GYDFTHYGMN 10

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Sequence Sequence Sequence

Sequence 3 Sequence 3 Sequence 3

Sequence Sequence Sequence Sequence

Sequence Sequence

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100.0%; Score 62; DB 4; Length 10; 100.0%; Pred. No. 0.0016;
                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 118M PC compatible
COMPUTER: 118M PC compatible
COMPUTER: 118M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-69-2002
CLASSIPICATION: CUNKNOWN:
PRIOR APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/12646
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/12646
FILING DATE: 06-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03.5ep-2002
CLASSIFICATION ATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REPERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 86: US-10-234-671-86
CITY: South San Prancisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 126, Application US/10234671
Publication No. USZ0030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GYDFTHYGMN 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AQC-1997
FILING DATE: 06-AQC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELEPONMUTCATION INFORMATION:
TELEPHONE: 650/22-1896
TELEPHONE: 650/25-9881
INFORMATION POR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                   APPLICANT: Baca. Manuel
APPLICANT: Bresta, Lames A.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Chen, Yoone M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
CUMTRY: USA
                                                                                                                                      Sequence 128, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 86, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-056-160B-128
                                                                                                                     US-09-056-160B-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-234-671-86
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TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYDFTHYGMN 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-974-591-126
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Sequence 18, Application Vo. US20040229310A1

Sequence 18, Application No. US20040229310A1

GENERAL INFORMATION: Lauran

TITLE SIMMONE, SAMMONE, LAURAN

TITLE OF INVENTION: WIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL

TITLE OF INVENTION: CULTURE

FILE OF INVENTION: CULTURE

FILE OF INVENTION: CULTURE

FILE OF INVENTION: CULTURE

SOFTON NUMBER: 2004-01-23

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PALENTH: 10

LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 62; DB 4; Length 10; 100.0%; Pred. No. 0.0016; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 62; DB 5; Length 10
100.0%; Pred. No. 0.0016;
Linnstohes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: YO117 VH HVR1 residues 26-35 US-10-764-428-18
    APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cul., Steven X.
REGISTRATION NUMBER: 44,637
REGISTRATION NUMBER: 91093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-9881
INPORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 aming acids
                                                                                                                                                                                                                                                                                                                                  TYPE: Amino Acid
TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-10-234-671-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 86, Application US/10974591
; Publication No. US20050112126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Publicant: Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-10-764-428-18
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Gaps
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NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM C compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM C compatible
COMPUTER: IBM C compatible
COMPUTER: IBM C compatible
COMPUTER: IBM C compatible
COMPUTER: IBM (Genentech)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P1093PlD1C1
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/974,591
PILING DATE: 26-Oct-2004
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/723752
PILING DATE: 27-NOV-2000
APPLICATION NUMBER: 08/908469
PILING DATE: 06-A00-1997
PILING DATE: 07-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 126, Application US/10974591
Publication No. US2005011216A1
GENERAL INFORMATION:
GAPPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
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JS-10-379-392-124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 62; DB 5; Length 10; 100.0%; Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/974,591
FILING DATE: 26-Oct-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/723752
FILING DATE: 27-NOV-2000
APPLICATION NUMBER: 08/908469
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/833504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8

US-10-379-392-58

Sequence 58, Application US/10379392

Publication No. US20040110226A1

GENERAL INFORMATION:

APPLICANT: Leazar, Gregory Alan

APPLICANT: Desiarlais, John Rudolf

APPLICANT: Desiarlais, John Rudolf

APPLICANT: Desiarlais, Ush Rudolf

APPLICANT: Daniyat, Bassil I.

TITLE OF INVENTION: ANTIBODY OPTIMIZATION

FILE REFERENCE: A-71386-3 463077-236

CURRENT APPLICATION NUMBER: US/0379,392

CURRENT FILING DATE: 2002-03-01

PRIOR FILING DATE: 2002-03-01

PRIOR FILING DATE: 2002-05-29

NUMBER OF SEQ ID NOS: 184

SOFTWARE: PATCHING DATE: 2002-05-29

NUMBER OF SEQ ID NOS: 184

SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
TOPOLOGY: Linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-10-974-591-126
                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 650/225-8674
TELEPAX: 650/952-981
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Humanized US-10-379-392-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Amino Acid
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Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Unknown
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RESULT 9 US-10-379-392-122

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100.0%; Pred. No. 0.018;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 62; DB 4; Length 117; Best Local Similarity 100.0%; Pred. No. 0.018; Matches 10; Conservative 0; Mismatches 0; Indels
Sequence 122, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71366-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT APPLICATION NUMBER: US 60/360,843
PRIOR APLICATION NUMBER: US 60/360,843
PRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SOFTWARE: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-10-379-392-124

i Sequence 124, Application US/10379392

i Publication No. US20040110226A1

i GENERAL INFORMATION:
    APPLICANT: Lazar, Gregory Alan
    APPLICANT: Desiarlais, John Rudolf
    APPLICANT: Desiarlais, John Rudolf
    APPLICANT: Desiarlais, John Rudolf
    APPLICANT: Desiarlais, Ush Rashil I.
    TITLE OF INVENTION: ANTIBODY OFTHWIZATION
    FILE REFERENCE: A-71386-3 463077-236
    CURRENT APPLICATION NUMBER: US/00/360, 843
    FRIOR APPLICATION NUMBER: US 60/360, 843
    PRIOR FILING DATE: 2002-03-01
    FRIOR FILING DATE: 2002-05-29
    NUMBER OF SEQ ID NOS: 184
    SOFTWARE: Patentin version 3.2
    SEQ ID NO 124
    LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-10-379-392-130
; Sequence 130, Application US/10379392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic US-10-379-392-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic
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Matches 10; Conservative
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0; Indels

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        100.0%; Score 62; DB 3; Length 118; 100.0%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 35. inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION DATA:
APPLICATION WHERE: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
RESTRENCE/DOCKET NUMBER: 28,616
RESTRENCE/DOCKET NUMBER: 29,616
RESTRENCE/DOCKET NUMBER: 29,616
RESTRENCE/DOCKET NUMBER: 20,616
RESTRENCE/DOCKET NUMBER: 20,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 116, Application US/09056160B
; Sequence 116, Application US/09056160B
; Patent No. US20020032315Al
; GENERAL INFORMATION:
    APPLICANT: Baca, Manuel
    APPLICANT: Presta, Leonard G.
    APPLICANT: Lowman, Henry B.
    APPLICANT: Comman, Henry B.
    APPLICANT: Comman, Henry B.
    APPLICANT: Comman, Henry B.
    APPLICANT: Comman, Henry B.
    APPLICANT: Avonne M.
    TILE OF INVENTION: ANTI-VEGF ANTIBODIES
    NUMBER OF SEQUENCES: 131
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                     REGISTRATION NUMBER: 28,616
REPERENCE/POCKET NUMBER: P109:
TELECOMMUNICATION INFORMATION:
TELERHONE: 650/225-1896
TELERRAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: 650/552-9881
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 118 amino acids
Amino Acid
                                                                                                                                                                                              LENGTH: 118 amino acida
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
  NAME: Hasak, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GYDFTHYGMN 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC_FEATURE
CCATION: (95)...(95)
CTHER INFORMATION: Xaa at position 95 can be Phe, Tyr or Met
US-10-379-392-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 62; DB 4; Length 117; 100.0%; Pred. No. 0.018;
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NAME/KEY: MISC FEATURE
LOCATION: (45)...(45)
OTHER INFORMATION: Xaa at position 45 can be Leu or Met
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 112, Application US/09056160B
Parent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Wells, James A.
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Daniyar, Bassil I.
TILLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT APPLICATION NUMBER: US 60/360,843
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SERO ID NO 130
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OFERTRAINS 1915AN: E. DOSJUE DESCRIPTION DATA:
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 10; Conservative
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26 GYDFTHYGMN 35

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: 35. inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/056,160B FILING DATE: 06-Apr-1998 CLASSIFICATION: 424 PRION APPLICATION MATE: 60/054,856 FILING DATE: 06-Aug-1997 ATTORNEY/AGENT INFORMATION: NAME: Hasak, Janet E. REGISTRATION NUMBER: 28,616 REGISTRATION NUMBER: 28,616 REGISTRATION NUMBER: 28,616 REGISTRATION NUMBER: 28,616 REGISTRATION NUMBER: P1093R2 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION SEQ ID NO: 118: 1 SEQUENCE GIRARACTERISTICS: 1 SEQUENCE G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 110, Application US/10234671
| Publication No. US20030190317A1
| GENERAL INFORMATION:
| APPLICANT: Baca, Manuel |
| Persera, Leonard G. |
| Persera, Leonard G. |
| Lowman, Henry B. |
| TITLE OF INVENTION: ANTI-VEGF ANTIBODIES |
| NUMBER OF SEQUENCES: 131 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSER: Genentech, Inc. |
| STREET: 1 DNA WAY |
| CITY: South San Francisco
                                                                                                                                                   APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                             ; Sequence 118, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
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US-09-056-160B-118
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US-10-234-671-110
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SCONFUTE RELIFECTION

COMPUTER READABLE FORM:

MEDIUM TIPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER READABLE FORM:

MEDIUM TIPE: 3.5 inch, 1.44 Mb floppy disk

COMBATHER INH FOCOMPATION:

SOFTWARE: Wilhearin (Generatech)

FILMS DATE: 0.3-Sep-2002

CURRENT APPLICATION MADRE: 0.8/10/234,671

FILMS DATE: 0.3-Sep-2002

MAPPLICATION NATURE: 0.6/12646

FILMS DATE: 0.3-Sep-1093

APPLICATION NATURE: 0.6/12646

FILMS DATE: 0.7-APP. 1997

APPLICATION NATURE: 0.6/12646

FILMS DATE: 0.7-APP. 1997

APPLICATION NATURE: 0.6/12646

MAMES CAL: SECOME N. 100-1997

APPLICATION NATURE: 0.6/12646

MAMES CAL: SECOME N. 100-1997

APPLICATION NATURE: 44,637

REFERENCE/POCKET NUMBER: 90/93R2CI

TELENCHMINING NOW SEN: 100.

FILMS SEQUENCE THANCATERISTICS:

INFORMATION FOR SEQ ID NO: 110:

SEQUENCE DESCRIPTION: SEQ ID NO: 110:

SEQUENCE DESCRIPTION: SEQ ID NO: 110:

MATCHES 10: Conservative 0; Mismatches 0; Indels 0; 0; Mismatches 0;
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April 25, 2006, 07:01:21 ; Search time 6.41509 Seconds (without alignments) 68.593 Million cell updates/sec
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1: /SIDS5/ptodata/1/pubpaā/US06_NEW_FUB.pep:*

2: /SIDS5/ptodata/1/pubpaa/US06_NEW_FUB.pep:*

3: /SIDS5/ptodata/1/pubpaa/US07_NEW_FUB.pep:*

5: /SIDS5/ptodata/1/pubpaa/PCT_NEW_FUB.pep:*

5: /SIDS5/ptodata/1/pubpaa/US10_NEW_FUB.pep:*

7: /SIDS5/ptodata/1/pubpaa/US10_NEW_FUB.pep:*

9: /SIDS5/ptodata/1/pubpaa/US11_NEW_FUB.pep:*

8: /SIDS5/ptodata/1/pubpaa/US11_NEW_FUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                             225428 seqs, 44002918 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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62
                                                                                                                                                                                                                                                                                                    1 GYDFTHYGMN 10
                                                                                                                                                                                                                                                        Title:
Perfect score:
Sequence:
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                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

					SUMMAKIES	
Regult No.	Score	Query Match	Query Match Length DB	08	aı	Description
-	62	100.0	118	٥	US-10-648-816-10	Sequence 10, Appl
8	62	100.0	118	9	US-10-648-816-12	
m	62	100.0	118	9	US-10-648-816-13	
4	62	100.0	121	9	US-10-648-816-16	
S	62	100.0	123	7	US-11-208-422-12	Sequence 12, Appl
9	51	82.3	256	-	US-11-054-515-2080	
7	51	82.3	256	7	US-11-266-444-2080	2080
8	48	77.4	92	7	US-11-240-195-84	84,
6	48	77.4	112	7	US-11-240-195-20	20,
10	48	77.4	116	7	US-11-174-186-2	ď
11	48	77.4	116	7	US-11-174-186-4	4
12	48	77.4	•	7	US-11-174-186-6	ģ
13	48	77.4	116	7	US-11-174-186-17	-
14	48	77.4		7	끄	
15	48	77.4		~	US-11-174-186-19	Sequence 19, Appl
16	48	77.4	_	7	US-11-174-186-20	
17	48	77.4	•	7	US-11-174-186-21	Sequence 21, Appl
18	48	77.4		7	11-174-	22,
19	48	77.4		7	US-11-174-186-23	Sequence 23, Appl
20	48	77.4		7	11-174-	Sequence 24, Appl
21	48	77.4	116	7	US-11-174-186-25	N
22	48	77.4		7	US-11-174-186-26	Sequence 26, Appl
23	48	77.4		7	US-11-174-186-35	Sequence 35, Appl
24	48	77.4		7	US-11-037-199-32	Sequence 32, Appl
25	48	77.4	118	9	US-10-648-816-9	Sequence 9, Appli

Sequence 14, Appl Sequence 15, Appl Sequence 7, Appl Sequence 31, Appl Sequence 11, Appl Sequence 111, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 58, Appl Sequence 58, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 54, Appl Sequence 53, Appl Sequence 68, Appl Sequence 68, Appl Sequence 68, Appl Sequence 69,	Sequence 848, App
US-10-648-816-14 US-10-648-816-15 US-11-240-195-7 US-11-240-195-7 US-11-240-195-111 US-11-240-195-111 US-11-240-195-111 US-11-240-195-110 US-11-240-195-109 US-11-240-195-109 US-11-240-195-109 US-11-240-195-109 US-11-104-590-53 US-11-116-250-58 US-11-116-250-58 US-10-512-184-31 US-10-512-184-71 US-10-512-184-70 US-11-054-515-848	=
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# ALIGNMENTS

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RESULT 1  US-10-648-816-10  Sequence 10, Application US/10648816  Sequence 10, Application US/10648816  PUBLICAN No. US2005244405A1  GENERAL INFORMATION:  APPLICANT: Van Bruggen, Nicholas  APPLICANT: Perrara, Mapoleone  TITLE OF INVENTION: And Uses Thereof  TITLE OF INVENTION: And Uses Thereof  TITLE OF INVENTION: And Uses Thereof  PILE REBERENCE: P1717D  CURRENT PELING DATE: 2003-08-26  PRIOR FILING DATE: 2003-08-26  PRIOR PILING DATE: 1998-12-22  PRIOR FILING DATE: 1998-12-22  PRIOR FILING DATE: 1998-12-22  NUMBER OF SEQ ID NOS: 16  SEQ ID NO 10  LENGTH: 118  TYPE: PRT  TYPE: PRT  COGANISM: Homo sapiens	Query Match 100.0%; Score 62; DB 6; Length 118; Best Local Similarity 100.0%; Pred. No. 0.00093; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 GYDFTHYGNN 10	RESULT 2 US-10-648-816-12 Sequence 12, Application US/10648816 Publication No. US20050244405A1 GENERAL INFORMATION: APPLICANT: Van Bruggen, Nicholas APPLICANT: Perrara, Napoleone TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists TITLE OF INVENTION: and Uses Thereof FILE REPRENCE: P117D1 CURRENT FILING DATE: 2003-08-26 PRIOR APPLICATION NUMBER: US/10/648,816 CURRENT FILING DATE: 2003-01-21 PRIOR APPLICATION NUMBER: US/09/718,694 PRIOR APPLICATION NUMBER: US/09/718,694 PRIOR PILING DATE: 1998-12-22

Gaps

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APPLICANT: Lien, Samantha

APPLICANT: Lien, Samantha

APPLICANT: Lien, Samantha

APPLICANT: Lowman, Henry B.

APPLICANT: Lowman, Henry B.

APPLICANT: Meng, Yu-Ju G.

TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
FILE REFERENCE: P21581

CURRENT APPLICATION NUMBER: US/11/208,422

CURRENT PILING DATE: 2005-08-19

PRIOR APPLICATION NUMBER: US 60/603,057

PRIOR PILING DATE: 2004-08-19

NUMBER OF SEQ ID NOS: 54

LENGTH: 123

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

FEATU
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US-11-054-51b-2080
US-11-054-51b-2080
US-11-054-51b-2080
Publication No. US2005025532A1
GENERAL INPORMATION:
I TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523B3
CURRENT PELING DATE: 2005-02-10
PRIOR PELING DATE: 2004-02-11
PRIOR PILING DATE: 2004-02-11
PRIOR PILING DATE: 2004-06-18
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
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Indels
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Mismatches
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                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/11208422
Publication No. US20060067930A1
GENERAL INFORMATION:
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10; Conservative
                                                                      1 GYDFTHYGMN 10
                                                                                                                                     26 GYDFTHYGMN 35
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Publication No. US2005024405A1

GENERAL INFORMATION:

APPLICANT: Van Bruggen, Nicholas

APPLICANT: Van Bruggen, Nicholas

APPLICANT: Perrara, Napoleone

TITLE OF INVENTION: and Uses Thereof

TITLE OF INVENTION: and Uses Thereof

FILE REFERENCE: P1717D1

CURRENT APPLICATION NUMBER: US/10/648,816

CURRENT PILING DATE: 2003-08-26

PRIOR PILING DATE: 2000-11-21

PRIOR PILING DATE: 1998-12-22

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 13

LENGTH: 118
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; Sequence 16, Application US/10648816
; Sequence 16, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Micholas
; APPLICANT: Perrara, Napoleone
; TITLE OF INVENTION: and USes Thereof
; TITLE OF INVENTION: and USes Thereof
; TITLE OF INVENTION: and USes Thereof
; TITLE OF INVENTION: 2003-08-26
; PRIOR PILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR PILING DATE: 2000-11-21
; PRIOR PILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 16
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                                                                                                                                                                                                                                                     100.0%; Score 62; DB 6; Length 118; 100.0%; Pred. No. 0.00093; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.00093;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 12
LENGTH: 118
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                                                                                                                                             ORGANISM: Homo sapiens US-10-648-816-12
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; ORGANISM: Homo sapiens
US-10-648-816-13
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Best Local Similarity
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ORGANISM:
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Jequence 20, Application US/11240195

Publication No. US20060057140A1

GENERAL INFORMATION:

APPLICANT: Feuerstein, Glora Z.

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT

TITLE OF INVENTION: OF THROMBOSIS

FILE OF PELICATION NUMBER: US/11/40,195

PRIOR FILING DATE: 2003-05-05

PRIOR PELING DATE: 1999-08-07

PRIOR PELING DATE: 1999-08-05

PRIOR PELING DATE: 1997-01-06

PRIOR PELING DATE: 1997-01-07

PRIOR PELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7; Length 92;
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                               PRIOR FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 09/344,050
PRIOR APLICATION NUMBER: 09/344,050
PRIOR APLICATION NUMBER: 08/783,853
PRIOR FILING DATE: 1997-01-06
PRIOR FILING DATE: 1997-01-06
PRIOR FILING DATE: 1996-01-17
PRIOR PILING DATE: 1996-01-17
PRIOR PILING DATE: 1996-10-24
NUMBER OF SEQ ID NOS: 111
SEQ ID NO 84
APPLICATION NUMBER: 10/051,852
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Best Local Similarity 80.0
Matches 8; Conservative
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23 GYTFTNYGMN 32
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ORGANISM: Homo sapiens
US-11-240-195-20
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CRGANISM: Homo sapiens
US-11-240-195-84
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| Sequence 2080, Application US/11266444
| Publication No. US20060062789A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICATY: Ruben et al. |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulate TILE REFERENCE: PF523PID1 |
| CURRENT FILING DATE: 2005-11-04 |
| FRIOR RAPPLICATION NUMBER: 09/880,746 |
| FRIOR PILING DATE: 2001-06-15 |
| FRIOR PILING DATE: 2000-06-16 |
| PRIOR FILING DATE: 2000-06-16 |
| PRIOR PILING DATE: 2000-06-16 |
| PRIOR PILING DATE: 2001-00-17 |
| PRIOR PILING DATE: 2001-03-16 |
| PRIOR PILING DATE: 2001-03-16 |
| PRIOR FILING DATE: 2001-05-25 |
| PRIOR FILING DATE: 2001-05-26 |
| PRIOR FILING DATE: 2010-05-26 |
| PRIOR FILING DAT
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| Sequence 84, Application US/11240195
| Publication No. US20060057140A1
| GENERAL INPORMATION:
| APPLICANT: Pewerstein, Giora Z. |
| TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT ITLE OF INVENTION: OF THROMBOSIS |
| TITLE OF INVENTION: OF THROMBOSIS |
| TITLE OF INVENTION: OF USERS. US/11/240,195 |
| GURRENT APPLICANTON NUMBER: US/11/240,195 |
| PRIOR APPLICATION NUMBER: US/10/430,176 |
| PRIOR APPLICATION NUMBER: 09/817,960 |
| PRIOR PRILING DATE: 2003-05-05 |
| PRIOR FILING DATE: 2001-03-27 |
| PRIOR FILING DATE: 1999-07-22 |
| PRIOR FILING DATE: 1999-07-22 |
| PRIOR FILING DATE: 1998-08-07 |
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                                                                                                                                                                                                                                  DB 7; Length 256;
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                                                                                                                                                                                                                                  Query Match 82.3%; Score 51; DB Best Local Similarity 80.0%; Pred. No. 0.15 Matches 8; Conservative 1; Mismatches
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         26 GYPFTHYGVN 35
                                                  ; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2080
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CRGANISM: Homo sapiens
US-11-266-444-2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-266-444-2080
                   SEQ ID NO 2080
LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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NAME/KEY: misc_feature
LOCATION: (85)...(85)
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OTHER INFORMATION: wherein Xaa at position 16 is a glutamic acid or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ## Seguence 4, Application US/11174186
## Publication No. US20050244418A1
## Seguence 4, Application US/11174186
## Publication No. US20050244418A1
## GENERAL INFORMATION:
## APPLICANT: Gillies, Stephen
## APPLICANT: Qian, Xiugi
## TILE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
## TILE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
## TILE OF INVENTION: RECOMBINANT APPLICATION NUMBER: US/11/174,186
## CURRENT APPLICATION NUMBER: US 60/288,564
## PRIOR FILING DATE: 2001-05-03
## NUMBER OF SEQ ID NOS: 42
## SOFTWARE: PatentIn version 3.3
## SEQ ID NO 4
## LEASTH: 116
RESULT 10
US-11-174-186-2
i Sequence 2, Application US/11174186
j Publication No. US20050244418A1
j GENERAL INFORMATION:
i APPLICANT: Gallies, Stephen
j APPLICANT: Qian, Xiugi
j TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
j TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
j TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
j FILE REPERENCE: LEX.019
j CURRENT FILING DATE: 2005-07-01
pRIOR PILING DATE: 2005-07-01
j PRIOR FILING DATE: 2005-05-03
j NUMBER OF SEQ ID NOS: 42
j SOFTWARE: Patentin version 3.3
j SBQ ID NO 2
l LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (2)...(2)
OTHER INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (9). [9)
OTHER INFORMATION: wherein Xaa at position 9 is a proline or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (11). (11)
OTHER INFORMATION: wherein Xaa at position 11 is a leucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: variable heavy chain sequence in the EpCAM antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.4%; Score 48;
80.0%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: KS VH mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GYDFTHYGMN 10
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GYTFTNYGMN 35
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NAME/KEY: misc_feature
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-174-186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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THER INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (69)...(69)
OTHER INFORMATION: wherein Xaa at position 69 is an alanine, a threonine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THER INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (80)...(80)
OTHER INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THER INFORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (46)..(46)
OTHER INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at position 68 is a phenylalanine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: wherein Xaa at position 83 is an isoleucine or a leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (84)7.(84)
OTHER INFORMATION: wherein Xaa at position 84 is an asparagine or a serine
                                                                                                                                                                                                                                                                 LOCATION: (40)..(40)
OTHER INFORMATION: wherein Xaa at position 40 is a threonine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an alanine or a threonine
LOCATION: (17)..(17)
OTHER INFORMATION: wherein Xaa at position 17 is a threonine or a serine
                                                                                                                                LOCATION: (38)...(38)
OTHER INFORMATION: wherein Xaa at position 38 is a lysine or an arginine
                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (43)...(43)
OTHER INFORMATION: wherein Xaa at position 43 is a lysine or a glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (71)..(71)

THER INFORMATION: wherein Xaa at position 71 is a serine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (72)...(72)
THER INFORMATION: wherein Xaa at position 72 is a leucine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an alanine or a leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (65)..(65)
OTHER INFORMATION: wherein Xaa at position 65 is a lysine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (76)..(76)
OTHER INFORMATION: wherein Xaa at position 76 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at position 79 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (68)..(68)
OTHER INFORMATION: wherein Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (79)...(79)
OTHER INFORMATION: wherein Xaa
                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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                                                                                               NAME/KEY: misc_feature
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FRATURE:
NAME/KEY: misc feature
LOCATION: (100)..(100)
OTHER INFORMATION: wherein Xaa at position 100 is an isoleucine or a methionine
                        FEATURE:
NAMB/KEY: misc_feature
LOCATION: (88)...(88)
OTHER INFORMATION: wherein Xaa at position 88 is an asparagine, an alanine or
OTHER INFORMATION: serine
                                                                                                                                                         FRATURE:
NAME/KBY: misc_feature
LOCATION: (91)...(91)
OTHER INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (108).
OTHER INFORMATION: wherein Xaa at position 108 is a glutamine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/11174186

| Sequence 6, Application US/11174186
| Publication No. US2005024418A1
| GENERAL INFORMATION:
| APPLICANT: Gillies, Stephen
| APPLICANT: Gillies, Stephen
| APPLICANT: Gillies, Stephen
| APPLICANT: Lax.olg
| TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
| TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
| TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
| TITLE OF INVENTION: UNDER: US/11/1/4,186
| CURRENT PILING DATE: 2001-05-03
| PRIOR FILING DATE: 2001-05-03
| NUMBER OF SEQ ID NOS: 42
| SEQ ID NOS: 42
| SEQ ID NOS: 42
| SEQ ID NOS: 42
OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; PEATURE: is NAME/KEY: misc feature; NAME/KEY: misc feature; LOCATION: (111)...(111); COTHER INFORMATION: wherein Xaa at position 111 is a serine or a threonine US-11-174-186-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ON: (2) \dots (4) INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
                                                                                                                                                                                                                                                                                                                LOCATION: (93)...(93)
OTHER INFORMATION: wherein Xaa at position 93 is a threonine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at position 9 is a proline or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (11)...(11)
OTHER INFORMATION: wherein Xaa at position 11 is a leucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 0.23;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (9)._(9)
OTHER INFORMATION: wherein Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYDFTHYGMN 10
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                                                                                                                                                                                                                                                  NAME/KEY: misc feature
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NAME/KEY: misc_feature
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LOCATION: (73)...(73)
OTHER INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic acid
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OTHER INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WAME/KEY: misc feature
COCATION: (80)...(80)
OTHER INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ION: (88). (88) in in a sparagine, an alanine or INFORMATION: wherein Xaa at position 88 is an asparagine, an alanine or INFORMATION: serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (63)..(63)
OTHER INFORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ION: (91)..(91). INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (68)...(68)
OTHER INFORMATION: wherein Xaa at position 68 is a phenylalanine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (46)..(46)
OTHER INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ION: (83)...(83)
INFORMATION: wherein Xaa at position 83 is an isoleucine or a leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (69)...(69)
OTHER INFORMATION: wherein Xaa at position 69 is an alanine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (76)...(76)
OTHER INFORMATION: wherein Xaa at position 76 is an alanine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (84)...(84)
OTHER INFORMATION: wherein Xaa at position 84 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (85)...(85)
OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (40)...(40)
OTHER INFORMATION: wherein Xaa at position 40 is a threonine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (93) ... (93) Try Order In Yaa at position 93 is a threonine or a valine PEATURE: NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (65)..(65)
OTHER INFORMATION: wherein Xaa at position 65 is a lysine or a glutamine
COCATION: (17)..(17)

THER INFORMATION: wherein Xaa at position 17 is a threonine or a serine
                                                                                                                                    LOCATION: (38)...(38)
OTHER INFORMATION: wherein Xaa at position 38 is a lysine or an arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (88)..(88)
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1 GYDFTHYGMN 10
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; LOCATION: (108)...(108); OTHER INFORMATION: wherein Xaa at position 108 is a glutamine or a threonine US-11-174-186-6
                                                                                                                                                                                                                                                                                                                         USECULATED TO SEQUENCE 17, Application US/11174186

Sequence 17, Application US/11174186

Publication No. US20050244418A1

GENERAL INFORMATION:

APPLICANT: Gillies, Stephen

APPLICANT: Gian, Xiugi

TILLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof

TILLE REPERRNCE: LEX-019

CURRENT APPLICATION NUMBER: US/11/174,186

CURRENT FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.3

SEQ ID NO 17

LENGTH: 116
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US-11-174-186-18
is Sequence 18, Application US/11174186
is Publication No. US20050244418A1
is GENERAL INFORMATION:
i APPLICANT: Gillies, Stephen
i APPLICANT: Qian, Xiugi
i TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
i TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
i FILE REFERENCE: LEx.019
i FULR REFERENCE: LEx.019
i FILE REPERENCE: US/11/174,186
i FILE REPERENCE: US/11/174,186
i FILE REPERENCE: US/11/174,186
i FILE REPERENCE: LEX.019
i PRIOR APPLICATION NUMBER: US 60/288,564
i PRIOR PILING DATE: 2001-05-03
i NUMBER OF SEQ ID NOS: 42
i SOCTANARE: Patentin version 3.3
i SEQ ID NO 18
i LENGTH: 116
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                                                                                           Query Match

77.4%; Score 48; DB 7; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels
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77.4%; Score 48; DB 7; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels
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26 GYTFTNYGMN 35
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ORGANISM: Artificial
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Best Local Similarity
Matches 8; Conserv
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ORGANISM: Artificial
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Gaps

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US-11-174-186-19
US-11-174-186-19
Sequence 19, Application US/11174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gaillies, Stephen
APPLICANT: Qian, Xiugi
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
TITLE OF INVENTION NUMBER: US/11/174,186
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT PILING DATE: 2005-07-01
PRIOR PILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3:3
SOFTWARE: Patentin version 3:3
SEQ ID NO 19
LENGTH: 116
TYPE PRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: VH2.5 heavy chain
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Matches 8; Conservative
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26 GYTPTNYGMN 35
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                      Copyright
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protein - protein search, using sw model Š

April 25, 2006, 06:05:16 ; Search time 58.7358 Seconds (without alignments) 82.286 Million cell updates/sec Run on:

US-10-764-428-19 64 Title: Perfect score:

1 GYSITSGYSWN 11 **BLOSUM62** Scoring table: Sequence:

2443163 seqs, 439378781 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequ2000s:* genesequ2001s:* genesequ2002s:* genesequ2003s:* genesequ2003s:* genesequ2004s:* geneseqp1980s:* geneseqp1990s:* A_Geneseq Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result		Query	, , ,	á	f	2000
Š.	Score	March	March Length UB	2 :	at .	neactification and transfer
-	64	100.0	11	80	ADQ90715	Adq90715 Anti-VEGF
(7	64	100.0	114	7	AAW95656	Aaw95656 Mus muscu
m	64	100.0	114	7	AAW95657	-
4	64	100.0	114	4	AAB76946	-
'n	64	100.0	114	4	AAB76945	Aab76945 Variable
9	64	100.0	114	œ	ADN07033	Adn07033 Anti-IgB
7	64	100.0	114	œ	ADN07032	Adn07032 Anti-IgE
60	64	100.0	114	σ	ADW00654	Adw00654 Human ant
0	64	100.0	114	6	ADW00655	
10	64	100.0	114	σ	ADW79890	•
11	64	100.0	114	6	ADW79889	Adw79889 Anti-IgE
12	64	100.0	119	e	AA020095	Aao20095 Protein e
13	64	100.0	121	~	AAW95647	Aaw95647 Mus muscu
14	64	100.0	121	~	AAW95648	_
15	64	100.0	121	4	AAB76936	0
16	64	100.0	121	4	AAB76937	Aab76937 Variable
17	64	100.0	121	80	ADN07024	Adn07024 Murine an
18	64	100.0	121	80	ADN07023	Adn07023 Murine an
19	64	100.0	121	σ	ADW00645	Adw00645 Murine Ma
20	64	100.0	121	σ	ADW00646	
21	64	100.0	134	~	AAR33306	Aar33306 MaB11 hea
22	64	100.0	134	m	AAY85194	Aay85194 Heavy cha
23	64	100.0	229	7	AAW95666	Aaw95666 Mus muscu
24	64	100.0	229	~	AAW95665	Aaw95665 Mus muscu

	Adn07067 F(ab) -pha Adn07042 Anti-1gE Adw00664 Human ant Adw00663 Human ant	Adw00689 Expressio Adw00694 Human ant Adw00693 Human ant Adw79899 Anti-IGE		Aab76960 Variable Adn07046 Anti-IgB Adn07047 Anti-IgB Adw00669 Human ant Adw00669 Human ant Adw79903 Anti-IgB
AAB76954 AAB76955 ADN07041	ADN07067 ADN07042 ADW00664 ADW00663	ADW00689 ADW00694 ADW00693	ADM 19899 ADM 19898 AAW95671 AAW95670	AAB76960 ADN07046 ADN07047 ADW00668 ADW00669 ADW00669
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25 26 27 6	28 29 30 31	1 S S S S	7 9 9 9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	) 4 4 4 4 4 4 10 4 10 10 4 10

# ALIGNMENTS

ADQ90715 standard; peptide; 11 AA.

21-OCT-2004 (first entry)

ADQ90715;

Anti-VEGF antibody heavy chain HVR1 peptide SEQ ID NO:19.

antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antiinflammatory; antianglogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; antiogenic disorder; immunological disorder; anti-VEGF antibody; anti vascular endothelial cell growth factor antibody; heavy chain; HVR1. 

Homo sapiens. Synthetic.

WO2004065417-A2.

05-AUG-2004.

23-JAN-2004; 2004WO-US001844.

23-JAN-2003; 2003US-0442484P.

(GETH ) GENENTECH INC.

Simmons L;

WPI; 2004-562149/54.

Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.

Claim 13; SEQ ID NO 19; 161pp; English.

The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid

cc the amino acid found at the corresponding FR position of a human subgroup variable domain consensus sequence that has a hypervatable region 1 (HVR1) and/or HVR2 amino acid sequence with the most sequence identity (HVR1) and/or HVR2 amino acid sequence with the most sequence identity with a corresponding HVR1 and/or HVR2 sequence of the variable domain.

CC The antibody or antigen binding fragment variable domain comprises the modified antibody or antigen-binding fragment. The antibody and antigen binding fragment to antibody and antigen binding fragment or antibody and antigen binding fragment in antibody and antigen binding fragment and antibody and antigen binding fragment invention are useful for methods and compositions of the present invention are useful for producing antibodies or antigen binding fragments in cell culture, in the particular for improving the yield of recombinant antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and composition and immunological disorders. The present sequence represents a heavy chain HVR1 peptide of an anti-VEGF (vascular cendothallal cell growth factor) antibody, which is used in the centure. ö Improving affinity of polypeptides, particularly anti-IgB antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the Variable heavy chain; IgB; antibody; anti-IgB; reduction; prevention; histenmine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic thinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria. Gaps ö Length 11; 0; Indels 100.0%; Score 64; DB 8; I 100.0%; Pred. No. 0.00063; Mus musculus anti-IgE e27 variable heavy chain. Lowe J; 0; Mismatches Disclosure; Page 90-91; 129pp; English. Jardieu PM, AAW95656 standard; protein; 114 AA. 98WO-US013410. 97US-00887352. (first entry) Best Local Similaring 1 GYSITSGYSWN 11 Lowman HB, Presta LG, (GETH ) GENENTECH INC. 1 GYSITSGYSWN WPI; 1999-106057/09. Sequence 11 AA; Mus musculus WO9901556-A2 30-JUN-1998; 02-JUL-1997; 08-JUN-1999 14-JAN-1999. AAW95656; Query Match RESULT 2 **AAW95656** ò

The sequence is that of the variable heavy chain of e27. It was used as part of a method to improve the affinity of anti-IgE antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgE mediated production of histamine in a mammal. They can be

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used for treating a disorder mediated by IgB such as hypersensitivity, atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Improving affinity of polypeptides, particularly anti-IgB antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                                                                                                                                                                                                                                                                                                  Variable heavy chain; IgB; antibody; anti-IgB; reduction; prevention; histenmine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.
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                                    eczema, anaphylactic shock and urticaria. The antil
for affinity purification, detection and diagnosis
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100.0%; Pred. No. 0.0083;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                          AAW95657 standard; protein; 114 AA.
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Les 11; Conserv
                                                                                                                                 Similarity
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                                                                                   Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                         08-JUN-1999
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Best Local S:
Matches 11
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Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.

Variable heavy chain sequence of e27 SEQ ID 11.

(first entry)

17-APR-2001

AAB76945;

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This invention relates to a nucleotide sequence encoding an antibody with improved anti-IgB antibody activity. The antibody has improved action due to a process comprising, a) identifying aspartyl residues prone to isomerisation in unimproved anti-IgB (immunoglobulin B) antibody; b) substituting alternative residues to create candidate molecules, and c) substituting alternative residues to create candidate molecules, and c) carget molecule. Use of the antibody results in antiasthmatic; antiallergic; ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IgB-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned concletc acids may also be used as affinity purification agents and in diagnostic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Anno acid sequences AAB76936.

AAB7660 represent fragments of anti-IgB antibodies of the invention. Polymucleotide sequence AAF69253 represents an expression plasmid used in the generation of affinity improved anti-IgB antibodies
                                                                                                                                                                                                                                                                                                                                                                    Antibody; antiaethmatic; antiallergic; ophthalmological; dermatological; antinflammatory; Ig B; immunoglobulin B; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding anti-immunoglobulin B antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin B prone to isomerization by other residues by affinity
                                                                                                                                                                                                                                                                                                   Variable heavy chain sequence of e25, e26 and e426 SEQ ID 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jardien PM,
                                                                AAB76946 standard; protein; 114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 2; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    maturation with phage display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00109207.
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                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-122353/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6172213-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-1998;
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                                                                                                                                                                                                                              17-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                 AAB76946;
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                                    AAB76946
ID AAB7
RESULT 4
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New nucleic acid encoding anti-immunoglobulin B antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin B prone to isomerization by other residues by affinity maturation with phage display.

Disclosure; Fig 2; 87pp; English.

Lowe J;

Jardieu PM,

Presta LG,

Lowman HB,

WPI; 2001-122353/13.

(GETH ) GENENTECH INC

02-JUL-1997; 30-JUN-1998;

98US-00109207. 97US-0051554P.

US6172213-B1 09-JAN-2001.

Synthetic.

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This invention relates to a nucleotide sequence encoding an antibody with improved anti-IgB antibody activity. The antibody has improved action due comprising, a) identifying aspartyl residues prone to isomerisation in unimproved anti-IgB (immunoglobulin B) antibody; b) substituting alternative residues to create candidate molecules, and c) substituting alternative residues which display affinity against the carget molecule. Use of the antibody results in antiasthmatic; antiallargic; ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IgF-mediated disorders cativity. The antibodies are useful for treating IgF-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned nucleic acids may also be used as affinity purification agents and in diagnostic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AAB76936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-1g8 antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-IgE antibody e25, e26 and e426 variable heavy chain domain (VH).
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100.0%; Pred. No. 0.0083;
ive 0; Mismatches 0; Indels
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nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GYSITSGYSWN 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 114 AA;
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Gaps

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11, Conservative 1 GYSITSGYSWN 11

Best Local Similarity Matches 11, Conserv

GYSITSGYSWN

8

AAB76945 standard; protein; 114 AA.

RESULT 5

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Region Region Region

Key

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Chemotherapy, IgB-mediated disorder; asthma; allergic rhinitis; eczema; urticaria; food allergy; hypersensitivity; anaphylactic hypersensitivity; antiasthmatic; antiallergic; dermatological; antibacterial; immune disorder; inflammation; ear disease; nose disease; throat disease; respiratory disease; antiinflammatory; dermatological disease; immunosuppressive; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                            New composition of an improved anti-IgE antibody or IgE binding fragment, useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to therapeutic compositions comprising anti-IgB antibody or IgB binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgB-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgB antibody variable heavy chain domain (VH).
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/note= "CDR (Complementarity-determining region)-H2"
99. 110
/note= "CDR (Complementarity-determining region)-H3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "CDR (Complementarity-determining region)-H1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human anti-IgB antibody e27 heavy chain variable region protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 64; DB 8;
100.0%; Pred. No. 0.0083;
                                                                                                                                                                                                                                                                                                                                          Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 11; 89pp; English.
                                                                                                                                                                                                                                                                                                                                          Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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26. .36
/label= CDR-H1
51. .66
                                                     /label= CDR-H2
                                                                                        /label= CDR-H3
                                                                                                                                                                                                                                             97US-0051554P,
98US-00109207,
                                                                                                                                                                                                          17-NOV-2000; 2000US-00716028
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                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-326922/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 114 AA;
                                                                                                                                                                                                                                             02-JUL-1997;
30-JUN-1998;
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                                                                                                                                 JS6723833-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition of an improved anti-1gB antibody or IgB binding fragment, useful for treating IgB-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgE antibody variable heavy chain domain (VH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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 Anti-IgB antibody; immunosuppressive agent; IgB-mediated disorder; therapy; atopic allergy; anaphylactic hypersensitivity; asthma; allergic rhintis; conjunctivitis; eczema; urticaria; food allergy; variable heavy chain domain; VH.
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100.0%; Pred. No. 0.0083;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-IgE antibody e27 variable heavy chain domain (VH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 12; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jardieu PM,
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                                                                                                                                   Location/Qualifiers
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/label= CDR-H1
51. .66
/label= CDR-H2
                                                                                                                                                                                                                                                 /label= CDR-H3
                                                                                                                                                                                                                                                                                                                                                                                                   97US-0051554P.
98US-00109207.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-326922/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-1998;
                                                                                                Unidentified
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                                                                                                                                                                                                                                                                                                                            20-APR-2004
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RESULT 7

Query Match

Matches

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4X8X4X4X4X4X4X4X4

Key

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Gaps

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Length 114; 0; Indels Lowe

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Antiasthmatic; Respiratory-Gen.; CNS-Gen.; Hypotensive; Antiinflammatory; Antimicrobial; Antiallergic; Cardiant; Analgesic; Vasotropic; asthma; chronic obstructive pulmonary disease; respiratory disease; pulmonary disease; respiratory disease; pulmonary bypertension; pulmonary spanea; emphysema; pulmonary hypertension; pulmonary fibrosis; hyperresponsiveness of the airways; infectious diseases; respiratory tract inflammation; chronic bronchitis; respiratory distress syndrome; pain; allergic rhinitis; cancer; immunoglobulin B; IgB; antibody; antibody therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-IgB antibody e26/e426/e25 heavy chain CDR domain fragment, SBQ ID 5.
                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for treating an IgB-mediated disorder. The method involves administering a therapeutical amount of an anti-IgB antibody or its IgB binding fragment. The invention is useful for treating an IgB-mediated disorder e.g. asthma, allergic rhinlis, eczema, utticaria, food allergies and hypersensitivity e.g. anaphylactic hypersensitivity. The present sequence is the human anti-IgB antibody e26, e27 and e426 variable heavy chain protein.
                                                                                                                                                                                                                                            Treating an IgB-mediated disorder, e.g. asthma, allergic rhinitis, eczema, urticaria, food allergies, or hypersensitivity, by administering an anti-IgB antibody or its antigen-binding fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 64; DB 9; Length 114; 100.0%; Pred. No. 0.0083; Pred. 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 12; 92pp; English.
                                                                                                                                                                   Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADW79890 standard; protein; 114 AA.
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                                     02-JUL-1997; 97US-0051554P.
30-JUN-1998; 98US-00109207.
17-NOV-2000; 2000US-00716028.
02-MAR-2004; 2004US-00791619.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
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                                                                                                                                                                      Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ball HA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROBI/) ROBINSON C B. (BALL/) BALL H A.
                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYSITSGYSWN
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                                                                                                                                                                                                           WPI; 2005-038757/04.
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Best Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-2005.
                                                                                                                                                                      Lowman HB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemotherapy, IgB-mediated disorder, asthma, allergic rhinitis, eczema, urticaria, food allergy, hypersensitivity, anaphylactic hypersensitivity; antiasthmatic; antiallergic, dermatological, antibacterial; immune disorder; inflammation; ear disease, nose disease; throat disease; respiratory disease; antimflammatory; dermatological disease; immunosuppressive; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for treating an IgB-mediated disorder. The method involves administering a therapeutical amount of an anti-IgB antibody or its IgB binding fragment. The invention is useful for treating an IgB-mediated disorder e.g. asthma, allergic rhinitis, eczema, urticaria, food allergies and hypersensitivity e.g. anaphylactic hypersensitivity. The present sequence is the human anti-IgB antibody e27 heavy chain variable region protein.
                                                                                                                                                                                                                                                                                                                                                               Treating an IgB-mediated disorder, e.g. asthma, allergic rhinitis, eczema, urticaria, food allergies, or hypersensitivity, by administering an anti-IgB antibody or its antigen-binding fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human anti-IgB antibody e26, e27 and e426 variable heavy chain protein.
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/note= "CDR (Complementarity-determining region)-H1"
51. .66
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                                                                                                                                                                                                                                                                                    Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 11; 92pp; English
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                                                                                                                                                                                                                                                                                    Jardien PM,
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                                                                                                                                                    02-JUL-1997; 97US-0051554P.
30-JUN-1998; 98US-00109207.
17-NOV-2000; 2000US-00716028.
                                                                                                              02-MAR-2004; 2004US-00791619
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                                                                                                                                                                                                                                                                                    Lowman HB, Presta LG,
                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                            WPI; 2005-038757/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                              US2004259077-A1.
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Query Match

Matches

ADW00655;

RESULT 9

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Region Region Region

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Gaps

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The present invention relates to compositions comprising a carrier, a first active agent comprising non-glucocorticoid servoids or their salts and a second active agent comprising an anti-immunoglobulin B (1gB) antibody effective to treat asthma, chronic obstructive pulmonary disease.

The compositions are also useful for ceducing the probability of or treating asthma and chronic obstructive pulmonary disease. The compositions are also useful for treating respiratory, lung/malignant disorder/condition such as asthma, chronic obstructive pulmonary disease, cystic fibrosis, dyspae, emphysema, chronic obstructive pulmonary hypertension, pulmonary fibrosis, hyper-responsive airways, increased adenosine or adenosine receptor levels, adenosine airways, increased adenosine or alengises, lung surfactant or usigninone depletion, chronic bronchitis, bronchoconstriction, difficult cuspiratory tract inflammation or allergies, lung surfactant or uniquinone depletion, chronic bronchitis, bronchoconstriction, difficult function, pulmonary vasoconstriction, impeded respiratory distress syndrome, administration of adenosine est for cardiac respiratory distress syndrome, administration of adenosine creation of adenosine creation of adenosine creation of adenosine or chronic bronchitis, and for reducing levels of sensitivity to adenosine or adenosine administration of adenosine pain, allergic rhinitis, cancer or chronic bronchitis, and for reducing levels of sensitivity to adenosine or adenosine creeptors. The present sequence is a humanized anti-IgB antibody CDR domain, used to illustrate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antiasthmatic; Respiratory-Gen.; CNS-Gen.; Hypotensive; Antiinflammatory; Antimicrobial; Antiallergic; Cardiant; Analgesic; Vasotropic; asthma; chronic obstructive pulmonary disease; respiratory disease; pulmonary disease; respiratory disease; pulmonary disease; cystic fibrosis; dyspnea; emphysema; pulmonary pypertension; pulmonary fibrosis; hypotrasponsiveness of the airways; infectious diseases; respiratory tract inflammation; chronic bronchitis; respiratory distress syndrome; pain; allergic rhinitis; cancer; immunoglobulin E; IgE; antibody; antibody therapy.
              Composition used for treating e.g. asthma, chronic obstructive pulmonary disease, cystic fibrosis, dyspnea, emphysema, pain, allergic rhinitis and cancer, comprises carrier, non-glucocorticoid steroids and anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-IgE antibody e27 heavy chain CDR domain fragment, SEQ ID 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                    immunoglobulin E antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 114 AA;
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The present invention relates to compositions comprising a carrier, a first active agent comprising non-glucocorticoid steroids or their salts and a second active agent comprising an anti-immunoglobulin B (IgE) antibody effective to treat asthma, chronic obstructive pulmonary disease.

Cor a respiratory or lung disease. The compositions are useful for crediting the probability of or treating asthma and chronic obstructive pulmonary disease. The compositions are also useful for treating respiratory, lung/malignant disorder/condition such as asthma, chronic obstructive pulmonary hypertension, pulmonary fibrosis, dyspaes, emphysema, chronic obstructive pulmonary hypertension, pulmonary bronchoconstriction, respiratory tract inflammation or allergies, lung surfactant or usiquinons depletion, chronic bronchitis, bronchoconstriction, difficult cusquinons depletion, chronic bronchitis, adenosine est for cardiac function, pulmonary vasoconstriction, impeded respiration, acute respiratory distress syndrome, pain, allergies crimitis, cancer or chronic bronchitis, and for reducing levels of sensitivity to adenosine or adenosine or adenosine or allergies antining antining contining and the present sequence of succerving the present sequence of succerving the present sequence is a humanized anti-IgB antibody CDR domain, used to illustrate the
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                                                                                                                  Composition used for treating e.g. asthma, chronic obstructive pulmonary disease, cystic fibrosis, dyspnea, emphysema, pain, allergic rhinitis and cancer, comprises carrier, non-glucocorticoid steroids and antimmunoglobulin E antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 64; DB 9; Length 114; 100.0%; Pred. No. 0.0083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by a 357nt DNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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nes 11; Conservative
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                                       Robinson CB, Ball HA;
                                                                                 WPI; 2005-161309/17.
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(BALL/) BALL H A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 114 AA;
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Length 119;

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The sequence is that of the variable heavy chain of MaEil. It was used as part of a method to improve the affinity of anti-IgE antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgE mediated production of histamine in a mammal. They can be used for treating a disorder mediated by IgE such as hypersensitivity, atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Improving affinity of polypeptides, particularly anti-1gB antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                       The invention relates to a changeable region of mouse monoclonal antibod recognising surface antigen preSI epitope of hepatitis B virus and gene. This sequence relates to a protein encoded by a 357nt DNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variable heavy chain; IgB; antibody; anti-IgB; reduction; prevention; histamine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.
                                                          Changeable region of mouse monoclonal antibody recognizing surface antigen preS1 epitope of hepatitis B virus and gene.
                                                                                                                                                                                                                                                            100.0%; Score 64; DB 3; Length 11
100.0%; Pred. No. 0.0087;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus anti-IgB MaB11 variable heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW95647 standard; protein; 121 AA.
                                                                                                             Disclosure; Page 12; 14pp; Korean.
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                                                                                                                                                                                                                                                                                                11; Conservative
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               2000-168375/15.
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                              N-PSDB; AAK99184
                                                                                                                                                                                                                               Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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Matches
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Lowe J;

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The sequence is that of the variable heavy chain of F(ab)-2. It was used as part of a method to improve the affinity of anti-1gB antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgB mediated production of histamine in a mammal. They can be used for treating a disorder mediated by IgB such as hypersensitivity, atopic allergy, asthma, allergy chinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Improving affinity of polypeptides, particularly anti-IgB antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                                                                                                                                                                      Variable heavy chain; IgB; antibody; anti-IgB; reduction; prevention; histamine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
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100.0%; Pred. No. 0.0088;
ive 0; Mismatches 0; Indel8
   Length 121;
                               0; Indels
                                                                                                                                                                                                                                                          Mus musculus anti-1gB F(ab)-2 variable heavy chain.
   Score 64; DB 2;
Pred. No. 0.0088;
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                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                     eczema; anaphylactic shock; urticaria.
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                                                                                                                                                                     AAW95648 standard; protein; 121 AA
    100.0%;
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                                                                                                                                                                                                                               (first entry)
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                                  Conservative
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                                                                                          26 GYSITSGYSWN 36
                                                                1 GYSITSGYSWN 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-106057/09.
Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
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Best Local £
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                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB76936
                                                                                                                                                          AAW95648
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                                                                                                                             antibody
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This invention relates to a nucleotide sequence encoding an antibody with improved anti-1gB antibody activity. The antibody has improved action due to a process comprising, a) identifying aspartyl residues prone to somerisation in unimproved anti-1gB (immunoglobulin B) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallergic; ophthalmological; dermatological and antiinflammatory cativity. The antibodies are useful for treating IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned nucleic acids may also be used as affinity purification agents and in diagnostic acids may also be used as affinity purification agents and in clasmostic acids may also be used as affinity purification agents and in clasmostic cell, tissues or serum. Amino acid sequences AAB76936-
ABA7690 represent fragments of anti-1gE antibodies of the invention.
Polynucleotide sequence AAF6923 represents an expression plasmid used in the generation of affinity improved anti-1gE antibodies
                                                                                                Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 64; DB 4; Length 121; 100.0%; Pred. No. 0.0088; Live 0; Mismatches 0; Indels
                                                            Variable heavy chain sequence of MaE11 SEQ ID 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jardieu PM, Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 1; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           maturation with phage display
                                                                                                                                                                                                                                                                                                                           98US-00109207,
                                                                                                                                                                                                                                                                                                                                                                   97US-0051554P.
                  17-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lowman HB, Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-122353/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1997;
                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                     US6172213-B1
                                                                                                                                                                                                                                                                                                                           30-JUN-1998;
                                                                                                                                                                                                                                                                                09-JAN-2001.
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$XCCCCCCCCCCCCCCX
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GYSITSGYSWN 36 1 GYSITSGYSWN 11 ò 유

11; Conservative

Matches

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Gaps ö

Search completed: April 25, 2006, 06:15:02 Job time : 60.7358 secs

Tue Apr 25 08:25:45 2006

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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sw model OM protein - protein search, using April 25, 2006, 06:15:41 ; Search time 9.33962 Seconds (without alignments) 113.322 Million cell updates/sec Run on:

US-10-764-428-19 64 1 GYSITSGYSWN 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	0 1	% Query Match	Length	80	TD.	Description
	2000			1		
1			11	-	HVMS1B	g heavy
8	58	90.6		N	S26467	g heavy chain
m	58	90.6		н	HVMS31	g heavy
4	28	0		~	B25114	g heavy chain
S	58	90.6	137	Н	AVMS35	g heavy
9	26	87.5		7	A25114	g heavy chain
7	26			~	830752	g heavy
· 00	54		-	~	859639	
σ	54	84.4		~	826464	g heavy
10	54	84.4		~	T01262	g heavy
11	7.0	84.4			838718	g heavy
12	53	82.8			836379	g heavy
13	53	87.8		~	128195	g heavy
14	52	81.2			F25114	g heavy
15	52	81.2		~	837200	g heavy
16	20	78.1		~	807454	heavy chain
17	49	76.6	135	N	PL0100	heavy
18	48	75.0		7	826902	heavy
19	48	75.0	98	~	S12421	heavy
20	48	75.0		~	D25114	g heavy
21	48	75.0			830530	heavy chain
22	48	75.0			S31673	chai
23	48	75.0	140		A24770	u
24	47	73.4			E70009	d hypot
25	46	71.9			C53285	g heavy
26	45	70.3			B24672	heavy chain pr
27	44	٠			C25114	g heavy cha
28	43	7.	91	7	S13689	g heavy cha
5	43	۲.			S13688	Ig heavy chain V r

Ig heavy chain V r Ig heavy chain V r	Ig heavy chain V r Ig heavy chain V r	apolipoprotein H-r probable potassium	probable oxidoredu	complement factor	ă	hypothetical prote		hypothetical prote	aldehyde-ferredox1	heparinase (BC 3.2	Ig heavy chain V r	Ig heavy chain V r
S13687 S13686	S13685 S07637	H35068	G70510	A35068	NBMSH	E70638	A84030	AD2545	A71221	JC7889	S26461	S14485
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67.2 67.2	67	69	9	65.6	65	64	62	62	62	62	19	61
4 43	43	4.4	4 4	42	42	41	40	40	40	40	39.5	39.5
30 31	35	) (f) (	0 0 0	37	38	39	40	41	42	43	44	4.5

### ALIGNMENTS

lg heavy chain precursor V region (1B43) - mouse

C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Date: Barly onset of somatic mutation in immunoglobulin VH genes during the primary
A;Reference number: JT0501; MUID:89279149; PMID:2499654
A;Accession: JT0508
A;Accession: JT0508
A;Accession: Translation not shown
A;Residues: 1-116 < LEV>
A;Acoss-references: UNIPROT:P18532; UNIPARC:UPI00000278E1
A;Experimental source: strain BALB/cJ
A;Coss-references: UNIPROT:P18532; UNIPARC:UPI00000278E1
A;Experimental source: strain BALB/cJ
A;Coss-references: unanuoglobulin
C;Superfamily: immunoglobulin V region; immunoglobulin
F;1-18/Domain: signal sequence #status predicted <AMT>
F;3-116/Domain: immunoglobulin homology <IMM>
F;3-116/Domain: immunoglobulin homology <IMM
F;3-116/Domain: immunoglobulin homology

Gaps ö Query Match

92.2%; Score 59; DB 1; Length 116;
Best Local Similarity 90.9%; Pred. No. 0.007;
Matches 10; Conservative 1; Mismatches 0; Indels

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Secret Secret C; Species: Mus musculus (house mouse) C; Species: Man musculus (house mouse) C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999 C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999 C; Accession: S26467 R; Kavaler, J. R; Reference number: S26459 A; Reference number: S26459 A; Status: preliminary A; Status: preliminary A; Rolecule type: mRNA A; Residues: 1-104 < KAV> A; Cross-references: UNIPARC: UPI0000115F5F; EMBL: X59105; NID: G51939; PIDN: CAA41831.1; PI C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Reywords: heterotetramer; immunoglobulin F; 6-89/Domain: immunoglobulin homology < IMM>

90.6%; Score 58; DB 2; Length 104; 90.9%; Pred. No. 0.0092; Query Match Best Local Similarity 2

**Begment** 

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A;MOlecule type: mRNA
A;Reaidues: 1-137 <RIN>
A;Cross-references: UNIPROT: P01822; UNIPARC: UPI000002727B; GB:M27638; NID:g602706; PIDN:
A; Title: Cloning, sequencing and expression of the rearranged MOPC 315 VH gene A; Reference number: PL0102; MUID:89238351; PMID:2497341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58; DB 1;
Pred. No. 0.012;
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                                                                                                                                                         A, Experimental source: strain MOPC 315
R, Rimfret, A.; Dorrington, K.J.; Klein, M.
submitted to the EMBL Data Library, June 1988
A, Reference number: 803262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
A25114
Ig heavy chain V region (HP22, HP27) - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A94484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYSITSGYSWN
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A93814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A91462
                                                                                                                                                                                                                                                                      A; Accession: S03262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: B25114
R; Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EXFOLIER, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EXFOLIER, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EXFOLIER, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
A; Accession: E25114
A; Reference number: A91028; MUID:86136012; PMID:3937730
A; Accession: E25114
A; Molecule type: mRNA
A; Residues: 1-119 < CLL>
A; Accession: E25114
A; Molecule type: mRNA
A; Residues: 1-119 < CLL>
A; Cross-references: UNIPARC:UPI0000115D24; GB:X03378; NID:G52007; FIDN:CAA27095.1; PID:GC; Superfamily: immunoglobulin immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology < LMM>
                                                                                                                                                                                                                                                                                                                                                                                                 during the primary
                                                                                                                                                                                                                                Ig heavy chain precursor V region (M315) - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C; Accession: JT0509
N; Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019; 1989
A; Title: Early onset of somatic mutation in immunoglobulin VH genes during the p A; Reference number: JT0501; MUID:89279149; PMID:2499654
A; Accession: JT0509
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-116 < LEV>
A; Mull C: Exp. Mull C: Exp.
A; C: Sexperimental source: strain BALB/CJ
C; Superfemily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-18/Domain: signal sequence #status predicted <NAT>F; 19-116/Product: Ig heavy chain V region (M315) #status predicted <MAT>F; 33-116/Domain: immunoglobulin homology < NMA>
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C;Species: 24-Apr-1984 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
C;Accession: PLO102; S03262; A93814; A91462; A93787; S23599
R;Rinfret, A.; Horne, C.; Dorrington, K.J.; Klein, M.
Mol. Immunol. 26, 431-434, 1989
        Gaps
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Pred. No. 0.011;
0; Mismatches 1; Indels
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Pred. No. 0.01;
        Indels
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        Mismatches
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Best Local Similarity 90.9
Matches 10; Conservative
     10; Conservative
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                                                         1 GYSITSGYSWN 11
                                                                                                        17 GYSITSGYYWN 27
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A; Molecule type: DNA
A; Residues: 1-15,'G', 16-137 <R12>
A; Residues: 1-15,'G', 16-137 <R12>
A; Cross-references: UNIPARC:UPI000016CE1C; EMBL:X07880; NID:g51760; PIDN:CAA30727.1; PID:
R;Jilka, R.L.; Pestka, S.
Proc. Natl. Acad. Sci. U.S.A. 74, 5692-5696, 1977
A;Title: Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin he A;Reference number: A93814; MUID:78094475; PMID:414225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Contents: annotation; revision to residue 53
R;Cheadle, C.; Hook, L.E.; Givol, D.; Ricca, G.A.
Mol. Immunol. 29, 21-30, 1992
A;Title: Cloning and expression of the variable regions of mouse myeloma protein MOFC315
A;Reference number: S23599; MUID:92114886; PMID:1731188
A;Accession: S23599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNA
*Residues: 19-137 «CHE»
A,Gross-references: UNIPARC:UPI0000113794; EMBL:X63972; NID:953532; PIDN:CAA45384.1; PID
C,Comment: This alpha chain was isolated from a myeloma protein that has anti-dinitrophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the heavy (alpha) chain of a mous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 19-52,'K',53-75,'BYGB',80-101,'D',103-106,'ZB',109-122,124-137 <FRA>
A;Residues: 19-52,'K',53-75,'BYGB',80-101,'D',103-106,'ZB',109-122,124-137 <FRA>
A;Rosi references: UNIPARC:UPI0000173740
R;Hood, L.; Margolies, M.; Givol, D.; Zakut, R.
unpublished results, cited by Padlan, B.A., Davies, D.R., Pecht, I., Givol, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;118,00main: signal sequence #status experimental <81G>
F;19-136/Product: Ig heavy chain V region (WOPC 315) #status experimental <WAT>
F;33-116/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-14, 'H', 16-31 <JIL>
A; Residues: 1-14, 'H', 16-31 <JIL>
A; Cross-references: UNIPARC: UD1000017373E
A; Note: the authors translated mRNA in vitro to obtain the precursor protein
R; Schechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.
Fed. Proc. 38, 1839-1845, 1979
A; Title: Structure and function of immunoglobulin genes and precursors.
A; Reference number: A91462; MUID: 79148758; PMID: 428562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 1, X', 3-11, X', 14-21 <SCH>
A; Residues: 1, X', 3-11, X', 14-21 <SCH>
A; Cross-references: UNIPARC:UPI00001737P
A; Oxose-references: UNIPARC:UPI00001737P
A; Note: the authors translated mand in vitro to obtain the precursor protein
R; Francis, S.H.; Leslie, R.G.G.; Hood, L.; Eisen, H.N.
Proc. Natl. Acad. Sci. U.S.A. 71, 1123-1127, 1974
A; Title: Amino-acid sequence of the variable region of the heavy (alpha) chain
A; Reference number: A93787; MUID:74170779; PMID:4524622
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A;Residues: 1-106 «KAV»
A;Residues: 1-106 «KAV»
A;Cross-references: UNIPARC:UP10000115F68; EMBL:X59114; NID:951926; PIDN:CAA41840.1; PIC
C;Superfamally: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3-86/Domain: immunoglobulin homology «IMM»
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C;Accession: T01262
R;Pirofski, L.A.; Thomas, B.K.; Scharff, M.D.
AiDS Res. Hum. Retroviruses 9, 41-49, 1993
A;Title: Variable region gene utilization and mutation in a group of neutralizing murin-A;Reference number: Z14285; Mulb: 7678971
A;Accession: T01262
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A;Molecule type: mRNA
A;Residues: 1-114 <PIR.
A;Residues: 1-114 <PIR.
A;Cross-references: UNIPARC:UPI0000117638; EMBL:S54194; NID:g264864; PIDN:AAB25246.2; P:C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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CjSpecies: Mus musculus (house mouse)
CjSpecies: Mus musculus (house mouse)
CjAccession: S38718
RjCimanis, A.Y.
submitted to the EMBL Data Library, November 1993
AjReference number: S38713
AjReference number: S38713
AjReference preliminary
AjRocession: S38718
AjRocession: S38718
AjRocession: S38718
                                                                                                                                                                                                                                                                                                                                                                                                                                             Tig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: 526464
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Accession: 526464
A;Accession: 526464
A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accessio
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Pred. No. 0.047;
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Pred. No. 0.044;
1; Mismatches
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Best Local Similarity 81.8
Local Similarity 91.8
Local Similarity 1.8
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Best Local Similarity 81.0
               9; Conservative
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                         C; Species: Mus musculus (house mouse)
C; Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jul-2000
C; Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jul-2000
C; Accession: A25114
EMBO J. 4, 3681-3688, 1985
A; Title: The idiotypic network and the internal image: possible regulation of a germ-lin A; Reference number: A91028; MUID:86136012; PMID:3937730
A; Accession: A22114
A; Molecule type: mRNA
A; Residues: 1-120 Coll.
A; Accession: Coll.
A; Accession: Vegion; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
C;Accession: 830752
R;Grant, P.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.
Nucleic Acids Res. 15, 5496, 1987
A;Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.
A;Reference number: 830751; MUID:87260030; PMID:3601683
A;Accession: 830752
A;Accession: 830752
A;Accession: S30752
A;Accession: S30752
A;Accession: MUID:87260030; PMID:3601683
A;Accession: S30752
A;Accession: MUID:87260030; MUID:9725256; PIDN:CAA29302.1; PII
C;Superfamily: immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
F;33-116/Domain: immunoglobulin homology <IMM>
F;33-116/Domain: c region (C-gamma 2b) (fragment) #status predicted <CRE>
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 15-Feb-196 #sequence_revision 01-Mar-1996 #text_change 17-Mar-1999
C; Accession: 859639
R; Boasart-Whitaker, P.; Chang, C.Y.Y.; Novotny, J.; Benjamin, D.C.; Sheriff, S.
J. Mol. Biol. 253, 559-575, 1995
A; Title: The crystal structure of the antibody NIO-staphylococcal nuclease complex at ; A; Reference number: 859639; MuID:96068846; PMID:7473734
A; Residues: preliminary
A; Residues: 1-106 <BOS>
A; Molecule type: mRNA
A; Residues: 1-106 <BOS>
A; Molecule type: mRNA
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroteramer; immunoglobulin
F; 8-91/Domain: immunoglobulin homology <INM>
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Pred. No. 0.023;
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81.8%; Pred. No. 0.044;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 23-Jul-1999

C; Accession: 636379; 833394

R; Ansell, K.H.

submitted to the EMBL Data Library, April 1993

A; Rosession: 836379

A; Rosession: 86787

A; Rosession: 8
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C; Species: Mus musculus (house mouse)
C; Date: 01-Dec-1999 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C; Accession: 128195
R; Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A; Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A; Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid & A; Reference number: A28195; MUID:88153717; PMID:3267217
A; Residues: 128195
A; Residues: 1-117 < SHE>
A; Residues: 1-117 < SHE>
A; Cross-references: UNIPARC:UPIO000114D72; GB:M19775; NID:g195526; FIDN:AAA38343.1; PID:A; Csesidues: the authors translated the codon AAC for residue 61 as Thr, and did not translath C; Repwords: heterotetramer; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin homology < IMM>
                                      PI
                          A;Cross-references: UNIPARC:UP1000117542; EMBL:X76018; NID:g416102; PIDN:CAA53605.1; C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                          Length 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53; DB 2; Length 59;
Pred. No. 0.035;
0; Migmatches 2; Indels
                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                  Score 54; DB 2;
Pred. No. 0.048;
1; Mismatches
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81.8%;
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Best Local Similarity
Matches 9; Conserva
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       A;Residues: 1-116 <CIM>
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Ig heavy chain V region (HP12) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: P25114
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Rougereau, M.
R;Ollier, P.; As6a-1368, 1985
A;Title: The idiotypic network and the internal image: possible regulation of a germ-lin A;Reference number: A91028, MUID:86136012; PMID:3937730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross_references. UNIPARC:UP10000115D28; GB:X03379; NID:g52013; PIDN:CAA27101.1; PID:g C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mENA
A;Mesiduss: 1-121 < FIS>
A;Residuss: 1-121 < FIS>
A;Cross-references: UNIPARC:UP100001161AC; EMBL:X74587; NID:g402639; PID:g402640
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S37200
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the RMED Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
A;Reference number: S37200
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Pred. No. 0.11;
0; Mismatches
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81.8%; Pred. No. 0.1;
iive 0; Mismatches
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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Matches 9; Conservative
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GYSITSEYAWN 36
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A; Residues: 1-115 <OLL>
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RESULT 1
HV61_MOUSE
ID HV61_MOUSE
AC P18532;
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Q53vq4 mus musculu
P18531 mus musculu
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                                                                                     April 25, 2006, 06:05:44 ; Search time 58.7358 Seconds (without alignments) 132.131 Million cell updates/sec
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P1831

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             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                  2166443 seqs, 705528306 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV61 MOUSE
Q53VQ4 MOUSE
HV60 MOUSE
HV60 MOUSE
Q53VQ5 MOUSE
Q53VQ5 MOUSE
Q53VR6 MOUSE
Q53VR7 MOUSE
Q559B8 RAT
Q559B8 RAT
Q559B8 RAT
Q559VQ1 MOUSE
Q53VQ1 MOUSE
Q53VQ2 MOUSE
Q53VQ2 MOUSE
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Q53VQ2 MOUSE
Q63VQ3 MOUSE
Q64VQ8 MOUSE
Q64VQ8 MOUSE
Q64VQ8 MOUSE
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Q8WQK6_PLAFA
Q8I2G4_PLAF7
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9CAUD
RHILV
MOUSE
DEIRA
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Maximum Match 100%
Listing first 45 summaries
                                                                 - protein search, using sw model
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Q61405
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Q857V7
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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64
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                                                                     OM protein
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        65.6
        498
        2
        Q588T9_EMENI
        Q558E9
        aspergillus

        33
        42
        65.6
        1234
        1
        CPAH_MÖUSE
        Q87018
        musculu

        34
        42
        65.6
        1234
        1
        CPAH_MÖUSE
        Q60599
        mus musculu

        36
        41
        64.1
        103
        2
        Q77Z79_MYCBO
        Q76279
        mycobacteri

        37
        41
        64.1
        103
        2
        Q4MYTZ9_MYCBO
        Q76219
        Mycobacteri

        39
        41
        64.1
        285
        2
        Q4MYT1_GIBZE
        Q4MYT1 gibberella

        40
        41
        64.1
        287
        2
        Q4KDEI_PSEPS
        Q4MVT1 gibberella

        40
        41
        64.1
        287
        2
        Q4KDEI_PSEPS
        Q5M4el pseudomonas

        40
        41
        64.1
        835
        2
        Q8GA49_ECOLI
        Q4MyTS
        Q4MpTS

        41
        41
        41
        43
        2
        Q4MPTS
        Q4MPTS
        Q5MSGA9
        escherichia

        43
        40.5
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# ALIGNMENTS

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RESULT. 1

HV61 MOURS

TH 66 MOURS

TH 66 MOURS

TO 1-800-1990 (Rel. 16, Last sequence update)

TO 10-800-1990 (Rel. 16, Last sequence update)

TO 1-800-1990 (Rel. 16
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NUCLEOTIDE SEQUENCE.
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REGION
REGION
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REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

11) TaxID=10090;
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                           92.2%; Score 59; DB 1; Length 116; 90.9%; Pred. No. 0.043;
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                                                                                                            0; Indels
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03378; CAA27096.1; -; mRNA.
                                                                           13158 MW; 1CB547253681FF74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       98 98
98 AA; 11202 MW; 4049CF8C7EE8AAE0 CRC64;
                                                                                                                                                                                                     13-58P-2005 (TrEMBLrel. 31, Created)
13-58P-2005 (TrEMBLrel. 31, Last sequence update)
13-58P-2005 (TrEMBLrel. 31, Last annotation update)
14 region (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Mus musculus (Mouse).
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                                                                                                            1; Mismatches
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                                                                                                                                                                                       OS3VQ4_MOUSE PRELIMINARY;
Q53VQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                             Conservative
                                                                                                                             1 GYSITSGYSWN 11
                                                                                                                                             44 GYSITSGYSWH 54
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                                                                  110
116 AA;
                                                                                                  Local Similarity
nes 10; Conserv
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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STRAIN=BALB/cJ;
MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86136012; PubMed=3937730; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                         PIR; JT0509; HVMS31.

PDB; 1EZV; X-ray; X=22-116.

SMR; P18531; 19-116.

Ensembl; ENSWUSGO0000057048; Mus musculus.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR003596; Ig_v.

SMART; SM00406; IG_v.

PROSTIR; PS50835; IG_LIKE; 1.

3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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Complementarity-determining-2.
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13095 MW; 4562E03E53DC9E10 CRC64;
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119 AA; 13931 MW; 502B51A5213F056B CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH-D-JH region (Fragment).
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90.9%; Pred. No. 0.063;
iive 0; Mismatches
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NOW TER 1 1 10
NOW TER 119 119
SEQÜENCE 119 AA; 13931 MW; SO2
                                                                                                    primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
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QS3VQ5;
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les 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8; MEDLINE-89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8; Rinfret A., Horne C., Dorrington K.J., Klein M.; "Cloning, sequencing and expression of the rearranged MOPC 315 VH gene seqment.";
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                              Gaps
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MEDLINE=79148758; PubMed=428562;
Schechter I., Wolf O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and precursors.";
Fed. Proc. 38:1839-1845(1979).
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Padlan B.A., Davies D.R., Pecht I., Givol D., Wright C.; Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANGOUS: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE OF 1-31.
MEDLINE=78094475; PubMed=414225;
Jilka R.L., Pestka S.;
"Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin heavy chain.";
Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
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Score 58; DB 2; Length 119;
Pred. No. 0.065;
                                              1; Indels
                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
pleavy chain V region MOPC 315 precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                  137 AA
                                                0; Mismatches
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Interpro; IPR007110; Ig-like.
Interpro; IPR003596; Ig_v.
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EMBL; X07880; CAA30727.1; -; Genomic_DNA
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      90.6%;
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    Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                             1 GYSITSGYSWN 11
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                                                                                                                                  26 GYSITSGYYWN
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HSSP; P01820; 1G7J.
SMR; P01822; 20-137.
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P01822;
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HV46 MOUSE
ID HV46 MC
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TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

KTISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

KTISSUE-Mammary tumor. WAP-TGF alpha model. 1.073/pnas.242603899;

RA KIAURDER R.D., Felngold B.A., Grouse L.H., Derge J.G.,

KIAURDER R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA HOPKINS R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Bigleton M.J., Usdin T.B., Toohiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Seters G.J., Malek J.A., Gunaratne P.H.,

RA Wordery K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Bakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,

R Generation and initial analysis of more than 15,000 full-length human mouse coll and coll and the references.
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                                                                                                                       Ig heavy chain V region MOPC 315. Pramework-1.
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Framework-4.
By similarity.
G -> GG (in Ref. 1; CAA30727).
G -> H (in Ref. 2).
G -> H (in Ref. 4).
N -> D (in Ref. 4).
Missing (in Ref. 4).
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Last annotation update)
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                                           birect protein sequencing, Immunoglobulin domain;
Immunoglobulin V region; Signal.
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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STRAIN=Mix FVB/N;
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STRAIN=Mix FVB/N;
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Name=LOC238447;
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Muridae; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
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Pred. No. 0.11;
1; Mismatches 1; Indels
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  TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
Submit X03375; CAA27078.1; -; mRNA.
EMBL; X03374; CAA27072.1; -; mRNA.
                       NIH MGC Project;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                      Immunoglobulin domain.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH-region (Fragment)
Mus musculus (Mouse).
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                                                    EMBL; BC002091; AAH02091.1; -; mRNA.
HSSP; P01820; 1G7J.
GO; GO:0003823; F:antigen binding; IEA.
GO; GO:003823; F:antigen binding; IEA.
InterPro; IPR003100; Ig_-11ke.
InterPro; IPR003597; Ig_-C1.
InterPro; IPR003596; Ig_-NHC.
InterPro; IPR003596; Ig_-NHC.
SMART; SW00406; IG_-NHC.
PROSTIE; PS50835; IG_-IKE; 4.
PROSTIE; PS50835; IG_-IKE; 4.
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81.8%;
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ID Q53VR7,

AC Q53VR7;

DT 13-SEP-2005 (TrEMBLrel. 31,

DT 13-SEP-2005 (TrEMBLrel. 31,

DT 13-SEP-2005 (TrEMBLrel. 31,
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QS3VR6;
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Best Local Similarity 81...
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10s 10; Conservative
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26 GYSITRGYNWN 36
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Carraine-FVBN N; TISSUB-Colon;

X STRAINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X Riausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Reference D.N., Marray M.N., Marra M.A.;

Reference D.N., Marray M.I., Marra M.A.;

Reference D.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Reference D.N., Marray D.M., Marra M.A.;

Reference D.N., Reference D.M., Marra M.A.;

Reference D.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Reference D.N., Marray D.M., Marra M.A.;

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Reference D.M., Marra D.M., Marra M.A.;

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bummalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Murcoidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                 WEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butherla, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03375; CAA27077.1; -; mRNA.
EMBL; X03374; CAA27071.1; -; mRNA.
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120 AA; 13892 MW; 013452306EBAA3BE CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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QSU413;
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26 GYSITRGYNWN 36
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InterPro; IPR003599; Ig.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Marinae; Rattus.
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                                                                            EMBL; BC085312, AAH85312.1; -; mRNA.

ENBEMD; ENSWUSG0000054328; Mus musculus.

GO, GO:003823; F:antigen binding; IEA.

InterPro; IPR00110; Ig-like.

InterPro; IPR003599; Ig-d.

InterPro; IPR003599; Ig-d.

InterPro; IPR003596; Ig-WHC.

InterPro; IPR003596; Ig-WHC.

InterPro; IPR003596; Ig-WHC.

INTERPRO; ISR00409; IG, 3.

SWART; SW00409; IG, 3.

SWART; SW00409; IG-MC; UNCXOWN 2.

PROSITE; PSS0835; IG_LIKE; 4.

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EMBL, BC092580; AAH92580.1; -; mRNA.
GO; GO:0003823; F:antigen binding; IEA.
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                                                         Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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81.8%;
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             STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q569B8_RAT PRELIMINARY;
Q569B8;
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13-SBP-2005 (TrEMBLrel. 31, Last sequence update)
13-SBP-2005 (TrEMBLrel. 31, Last annotation update)
13-SBP-2005 (TrEMBLrel. 31, Last annotation update)
Wh region (Fragment)
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Burchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Glires, Rodentía, Sciurognathi;
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                                                                                                                                                                                                                                                                                             82.8%; Score 53; DB 2; Length 590;
81.8%; Pred. No. 2.5;
ive 0; Mismatches 2; Indels
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Pred. No. 0.54;
0; Mismatches 2; Indels
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03379; CAA27102.1; -; mRNA.
NON_TER 1
                  InterPro; IPR03597; Ig cl.
InterPro; IPR03597; Ig cl.
InterPro; IPR03596; Ig v.
Pfam; PP07654; Ig v.
Pfam; PP07654; IG set; 4.
SWART; SW00409; IG; 2.
SWART; SW00407; IGcl; 4.
SWART; SW00406; IGv; 1.
PROSITE; PS00290; IG LIKE; 5.
PROSITE; PS00290; IG LIKE; 5.
PROSITE; PS00290; IG LIKE; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 AA; 11191 MW; B3585BB6P080616 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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81.8%;
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Q53VQ1;
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.0.
Best Local Similarity 81.0.
Conservative
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InterPro; IPR007110;
InterPro; IPR003597;
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VH-D-JH region (Fragment).
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                                          Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Matches 8; Conserv
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                                 MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murines; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; "The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
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                                                                                                                                                                                                        81.2%; Score 52; DB 2; Length 115; 81.8%; Pred. No. 0.65;
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                                                                                                                                                                                                                                 2; Indels
                                                                                                                                      Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03379; CAA27101.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03377; CAA27090.1; -; mRNA.
NON_TER
                                                                                                                                                                                  115 AA; 13257 MW; D465A5854DF459A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                         13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Last annotation update)
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MEDLINE=86136012; PubMed=3937730;
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                                                                                                                  NUCLEOTIDE SEQUENCE OF 28-29
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Q53VQ9
13-SEP-2005 (TEMBLFel. 31,
13-SEP-2005 (TEMBLFel. 31,
13-SEP-2005 (TEMBLFel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                  Q53VQ8 MOUSE PRELIMINARY;
Q53VQ8;
                                                                                                                                                                                                                   Best Local Similarity 81.8 Matches 9; Conservative
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                                                                                                                                                                                                                                                       1 GYSITSGYSWN 11
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                                                                                                                                                                                                                                                                                                                                                                                             VH region (Fragment)
Mus musculus (Mouse)
  NCBI_TaxID=10090;
                                                                                                                             Fougereau M.;
Submitted (NO)
                         NUCLEOTIDE
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SEQUENCE
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MEDLINE=86136012; PubMed=3937730;

Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;

Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;

"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";

EMBO J. 4:3681-3688(1985).
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Hilbert H., Duesterhoeft A., Pohl T.M., Weitzenegger T.;
"Analysis of the Bacillus subtilis genome: cloning and nucleotide
sequence of a 62 kb region between 275 degrees (rrnB) and 284 degrees
Mus musculús (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Broulllet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.
Entian K.-D., Errington J., Fabret C., Ferrari B., Foulger D.,
Ghim S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03377; CAA27089.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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01-011-1997 (TrEMBLrel. 04, Last sequence update)
01-011-1997 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein yufp.
Name=yufp; OrderedLocusNames=BSU31560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.0%; Score 48; DB 2; 72.7%; Pred. No. 3.2;
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1; Mismatches
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005254; 0795M0;
01-JUL-1997 (TrEMBLrel. 06
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RA Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,

A Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M.,

RA Klein C., Kobayashi Y., Koetter P., Komingstein G., Krogh

R. Kuano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,

R. Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,

RA Medique C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,

RA Meback M., Noone D., O'Serliy M., Ogwara K., Ogwara A., Oudega B.,

RA Perscott A.M., Presecan B., Pujic P., Purnelle B., Rapoport G.,

RA Rey M., Raynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,

RA Rey M., Sadaie Y., Sato T., Scheleich S., Schroeter R.,

RA Rose M., Sadaie Y., Sato T., Scholita C., Roche B.,

RA Rose M., Sadaie Y., Sato T., Schoska A., Serro P.,

RA Rose M., Sadaie Y., Sato T., Schoska A., Serro P.,

RA Rose M., Sadaie Y., Sato T., Schoska A., Serro P.,

RA Togmoni A., Tosato V., Uchiyama S., Vandenbol M., Taraka T., Tarakashi H.,

RA Togmoni A., Tosato V., Uchiyama S., Vandenbol M., Yamane K.,

RA Meltersoger T., Winters P., Wipat A., Yamanoto H., Yamane K.,

RA Meltersoger T., Winters P., Wipat A., Yamanoto H., Yamane K.,

RA Meltersoger T., Winters P., Wipat A., Yamanoto H., Yamane K.,

RA Yoshikawa H., Danchin A.;

RA Yoshikawa H., Danchin A.;

RA Meltis S. Soldo B., Sorchikawa H.-F., Zumetein B.,

REMBL; 23912; CABN318.1; -; Genomic DNA.

BR REBL; 20912; CABN318.1; -; Genomic DNA
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Search completed: April 25, 2006, 06:24:35 Job time : 61.7358 secs

1 GYSITSGYS--WN 11 |||: |||| || 30 GYSVASGYSALWN 42

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Query Match
Best Local Similarity 100.
Matches 11; Conservative
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US-08-887-352B-12
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US-08-887-352B-11
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                                                                                                                                April 25, 2006, 06:25:05; Search time 14.8396 Seconds (without alignments) 61.284 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Sequence 12, Sequence 12, Sequence 11, Sequence 11, Sequence 11, Sequence 12, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 12, Sequence 12, Sequence 12, Sequence 12, Sequence 12, Sequence 2, A
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Sequence 2,
Sequence 3,
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Sequence 3,
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Sequence 2,
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                       GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6_COMB.pep:*
(cgn2_6/ptodata/1/iaa/H_COMB.pep:*)
(cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*)
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*)
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US-09-206-005-11

US-09-206-005-12

US-09-20-171-11

US-09-716-028-11

US-09-716-028-11

US-10-113-996-11

US-10-113-996-11

US-09-716-028-12

US-09-109-207C-2

US-09-109-207C-3

US-09-206-005-3

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                                                                                                                                                                                                                                                                                                                                              572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gB Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides

NUMBER OF SECURICES:

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 1 DAN Way

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                               Sequence 21,
Sequence 20,
Sequence 21,
Sequence 21,
Sequence 21,
Sequence 21,
Sequence 21,
                                                                                                                                                                       Sequence Sequence Sequence S
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ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,3528
FILING DATE: 03-U1-1997
CLASSIFCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 91123
TELECOMMUNICATION INFORMATION:
TELEFHONE: 650/25-1489
TELEFHONE: 650/25-1489
TELEFHONE: 650/25-1489
TELEFHONE: GSO/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
US-09-802-077-3
US-09-925-179-3
US-08-887-352B-21
US-08-887-352B-21
US-09-109-207C-20
US-09-109-207C-21
US-09-226-005-21
US-09-220-171-20
US-09-320-171-21
US-09-920-171-21
US-09-920-171-21
US-09-920-171-21
US-09-920-171-21
US-09-116-028-21
US-10-113-996-21
US-10-113-996-21
US-08-887-352B-25
US-08-887-352B-25
US-08-109-207C-25
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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-3528-11
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Gaps

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APPLICANT: Henry B. Lowman, Leonard G. Presta, Faula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide FILE REFERENCE: P112381
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR RILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 12
LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides FILE REFERENCE: P1123C1r
CURRENT APPLICATION VOYSE: US/09/296,005
CURRENT PILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 11
LENGTH: 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-109-207C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Artificial CCATION: 1-114 CTHROWATION: Heavy chain sequence derived from MAE11 (15-09-296-005-11)
                                                                                                                                                                                   Sequence 12, Application US/09109207C Patent No. 6172213 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/09296005
Patent No. 6290957
GENERAL INFORMATION:
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US-09-296-005-12
Sequence 12, Application US/09296005
; Patent No. 6290957
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Best Local Similarity 100.
Matches 11; Conservative
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Sequence 11, Application US/09109207C

Sequence 11, Application US/09109207C

Sequence 11, Application US/09109207C

Sequence 11, Application US/09109207C

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe FILE REFERENCE: P1123R1

CURRENT APPLICANTION NUMBER: US/09/109,207C

CURRENT FILING DATE: 1999-06-30

PRIOR FILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 11

LENGTH: 114
Sequence 12, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgB Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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COTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-11
                                                                                                                                                                                                                                                                                                                               COUNTY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinEatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPHONE: 650/225-1489
TELEPHONE: 650/25-1489
TELEPHONE: GOS/55-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 114 amino acids
Amino Acid
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Best Local Similarity 100.
Matches 11, Conservative
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ORGANISM: Artificial
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US-08-887-352B-12
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial
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US-09-716-028-12
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GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gB Antibodies and Method of Improving Polypeptides
TITLE BOF INVENTION: Improved Anti-1gB Antibodies and Method of Improving Polypeptides
TITLE NOT APPLICATION NUMBER: US/09/296,005
CURRENT APPLICATION NUMBER: US 08/887,352
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER APPLING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 12
SEQ ID NO 12
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US-09-20-171-11
Sequence 11, Application US/09920171
Sequence 11, Application US/09920171
Sequence 11, Application US/09920171
Sequence 11, Application US/09920171
Sequence 11, Application:
AppliCANT: Lowent Henry B.
APPLICANT: Lowent Henry B.
APPLICANT: Lowent Henry B.
APPLICANT: Lowent Henry B.
APPLICANT: Lowent John
TILE REFERENCE: P1123C2US
FILE REFERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
PRIOR FILING DATE: 1997-04.
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR PRIOR DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 11
LENGTH: 114
TTYPE: PRT
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| Sequence 12, Application US/09920171
| Sequence 12, Application US/09920171
| Patent No. 6682735
| Patent Norman, Henry B.
| APPLICANT: Lowman, Henry B.
| APPLICANT: Presta, Leonard G.
| APPLICANT: Lowe, John M.
| APPLICANT: Lowe, John Paula M.
| TITLE OF INVENTION: Improved Anti-IgB Antibodies (as amended)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 114;
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                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Heavy chain sequence derived from MAB11
US-09-296-005-12
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100.0%; Pred. No. 0.0043;
tive 0; Mismatches 0
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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09/920,171

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PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 09,
NUMBER OF SEQ ID NOS: 44
LENGTH: 114
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Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                               ; LOCATION: 1-114; OTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-716-028-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-11
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Sequence 12, Application US/10113996

Patent No. 6761889

GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Jardieu, Faula M.
APPLICANT: Lowe, John
TITLE OP INVENTION: Improved Anti-IgE Antibodies
FILE REFERRICE: P11230308

CURRENT FILING DATE: 2002-04-01

PRIOR PILING DATE: 1997-07-02

PRIOR APPLICATION NUMBER: US 08/887,352

PRIOR PLING DATE: 1997-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/10113996
Patent No. 6761889
GENERAL INFORMATION:
GAPLICANT: Lowen, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVERTION: Improved Anti-IGE Antibodies
FILE REPERENCE: P1123C3US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/113,996
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1997-04-21
PRIOR PILING DATE: 1999-04-21
PRIOR PILING DATE: 2099-04-21
PRIOR PILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 11
LENGTH: 114
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      NUMBER OF SEQ ID NOS: 44
                                                                                                       FEATURE:
NAME/KEY: Artificial
                                                                                    ORGANISM: Artificial
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                       SEQ ID NO 12
LENGTH: 114
                                                                 TYPE: PRT
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improving Polypeptides
TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITT: South San Francisco
STREET: California
COUNTRY: USA
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                                                                                                                  Query Match 100.0%; Score 64; DB 2; Length 114; Best Local Similarity 100.0%; Pred. No. 0.0043; Matches 11; Conservative 0; Mismatches 0; Indels
                                        ; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/887,352B FILING DATE: 03-Jul-1997 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: SYODOGA, CTALG G. REGISTRATION NUMBER: 39,044 REFERENCE/DOCKET NUMBER: 91,044 REFERENCE/DOCKET NUMBER: 91,044 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-887-352B-3
; Sequence 3, Application US/08887352B
; Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08887352B; Patent No. 5994511
ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
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US-08-887-352B-2
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Job time : 15.8396 secs
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improving Polypeptides and Method of TITLE OF INVENTION: Improving Polypeptides and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBERS OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE Genentech, Inc.
CYRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE Genentech, Inc.
CYRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE Genentech, Inc.
COUNTRY: USA
ZIF SOUTH AND FORM: PC-DOS/MS-DOS
CONTRY: USA
ZIP: 94080
COMPTER IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: OS-DOS/MS-DOS
SOFTWARE: Winfeatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-301-1997
CLASSIFICATION NUMBER: 930-044
REFERENCE/DOCKET NUMBER: P1123
TELEROMMUNICATION INFORMATION:
TYPE: AMAIO Acid
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US-09-109-207C-2
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Sequence 2, Application US/09109207C

Requence 2, Application US/09109207C

Patent No. 6172213

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TILLE OF INVERTION: Improved Anti-1gR Antibodies and Method of Improving Polypeptide PILE REPERENCE: P1123R1

CURRENT APPLICATION WUMBER: US/09/109,207C

CURRENT PILING DATE: 1998-06-30

PRIOR FILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 2

LENGTH: 121 ö 0; Gapa 100.0%; Score 64; DB 2; Length 121; 100.0%; Pred. No. 0.0045; tive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 11; Conservative 1 GYSITSGYSWN 11 26 GYSITSGYSWN 36 ) ORGANISM: Mus musculus US-09-109-207C-2 ò 셤

Search completed: April 25, 2006, 06:28:38

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SQUENCE TO THE PARTICAL OF US20040229310A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WETHOOS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING TITLE OF INVENTION: CULTURE OF INVENTION: CULTURE OF INVENTION: CULTURE OF INVENTION: US-120/764,428

TITLE REPERENCE: 11669-12005U1

CURRENT APPLICATION NUMBER: US 60/442,484

PRIOR PRILING DATE: 2003-01-23

PRIOR PRILING DATE: 2003-01-23

NUMBER OF SEQ ID NOS: 33

SOPTWARE: Patentin version 3.1
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Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels
US-09-920-171-25
US-09-920-171-26
US-10-113-996-25
US-10-113-996-25
US-10-791-619-25
US-10-698-073-19
US-10-698-073-19
US-09-920-171-22
US-09-920-171-23
US-10-113-996-23
US-10-113-996-23
US-10-791-619-23
US-10-791-619-23
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US-10-698-073-16
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US-10-764-428-19
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ORGANISM: Artificial Sequence
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     GYSITSGYSWN 11
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US-09-920-171-11
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LENGTH: 11
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113, Appl
114, Appl
115, Appl
116, Appl
117, Appl
118, Appl
119, A
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                                                                                                                                   April 25, 2006, 06:58:17 ; Search time 47.9434 Seconds (without alignments) 95.866 Million cell updates/sec
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Sequence 11,
Sequence 12,
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Sequence 4, A
Sequence 5, A
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/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                            GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-113-996-11
US-10-113-996-12
US-10-791-619-12
US-10-791-619-12
US-10-791-619-12
US-09-920-171-3
US-09-920-171-3
US-10-113-996-2
US-10-113-996-2
US-10-791-619-2
US-10-791-619-3
US-09-802-077-3
US-09-802-077-3
US-09-920-171-20
US-09-920-171-20
US-10-113-996-21
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                                                                                                                                                                                                                                                                                                                                          1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Gaps

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TYPE: PRT ORGANISM: Artificial
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US-10-791-619-11
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SEQ ID NO 11
LENGTH: 114
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GENERAL INCOMMATION:

APPLICANT: LOWARION:

APPLICANT: Presta, Leonard G.

APPLICANT: Jordeu, Paula M.

APPLICANT: Jordeu, Paula M.

TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)

FILE REFERENCE: 1123C2US

CURRENT APPLICATION NUMBER: US/09/920,171

CURRENT FILING DATE: 2001-08-01

PRIOR FILING DATE: 1997-07-02

PRIOR FILING DATE: 1999-04-21

FRIOR FILING DATE: 1999-04-21

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 12
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                                                                                                          FEATURE:
; CTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAB11
US-05-920-171-12
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APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies
FILE REFERENCE: P1123G3US
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CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR PILING DATE: 1999-04-21
PRIOR PILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 09/920,171
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 44
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Publication No. US20030149244A1
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09920171 Patent No. US20020054878A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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      NUMBER OF SEQ ID NOS: 44
SEQ ID NO 11
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/10/791,619
CURRENT APPLICATION NUMBER: US/09/109,207
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1999-06-30
PRIOR PILING DATE: 1999-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 11
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100.0%; Score 64; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                     Query Match 100.0%; Score 64; DB 4; Length 114; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 11; Conservative 0; Mismatches 0; Indels
                                                    ; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-12
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/10113996
; Sequence 12, Application US/1011396
; Publication No. US2003014924A1
; GENERAL INCRNATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; CURRENT PELICATION NUMBER: US/10/113,996
; CURRENT PILING DATE: 2002-04-01
; PRIOR FILING DATE: 1999-07-02
; PRIOR FILING DATE: 1999-04-21
; PRIOR FILING DATE: 1999-04-21
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
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ORGANISM: Artificial Sequence
TYPE: PRT
ORGANISM: Artificial Sequence
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; GARMARHI LINCUALITY.

APPLICANT: ROBINSON, CYNTHIA B.

APPLICANT: ROBINSON, CONTHIA B.

APPLICANT: ROBINSON, COMBINATION OF DEHYDROEPIANDROSTERONE OR

TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OF TITLE OF INVENTION: BUTHORNY DISEASE

TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE

TITLE OF INVENTION: PULMONARY DISEASE

TITLE OF INVENTION: PULMONARY DISEASE

TITLE OF INVENTION: PULMONARY DISEASE

CURRENT PLILING DATE: 2003-10-26

PRIOR APPLICATION NUMBER: 60/492,231

PRIOR PLILING DATE: 2003-07-31

NUMBER OF SEQ ID NOS: 19

SEQ ID NO 5

LENGTH: 114
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| Sequence 2, Application US/09920171
| Patent No. US20020054878A1
| GENERAL INFORMATION:
| APPLICANT: Lowen, Henry B.
| APPLICANT: Dardieu, Paula M.
| APPLICANT: Lowe, John
| TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
| FILE REFERENCE: P1123C2US
| CURRENT PILING DATE: 2001-08-01
| CURRENT PILING DATE: 2001-08-01
| PRIOR FILING DATE: 1997-07-02
| PRIOR FILING DATE: 1997-04-21
| NUMBER OF SEQ ID NOS: 44
| SEQ ID NO 2
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Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                          Query Match
100.0%; Score 64; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels
; OTHER INFORMATION: Humanized Monoclonal Antibody
US-10-698-073-4
                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10698073 Publication No. US20050026881A1 GENERAL INFORMATION:
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US-09-920-171-2
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Sequence 12, Application US/10791619

Publication No. US20040259077A1

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

TITLE OF INVENTION:

CURRENT PELICATION NUMBER: US/10/791,619

CURRENT PAPLICATION NUMBER: US/09/109,207

PRIOR PAPLICATION NUMBER: US 60/051,554

PRIOR FILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-06-30

SRIOR PILING DATE: 1998-06-30

SRIOR PILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 44

TYPE: PRI

CURRENT: 114

TYPE: PRI

SROWISM: Artificial

SRAMISM: Artificial
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; Sequence 4, Application US2005026881A1
; Beblication No. US20050026881A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: WIGHER: US/10/698,073
; CURRENT PILING DATE: 2003-10-26
; PRIOR PILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTHARE: PATENTIN Ver. 3.2
; SEQ ID NO 4

LENGTH: 114
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Pred. No. 0.011;
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LOCATION: 1-114

COTHER INFORMATION: Heavy chain sequence derived from MAE11

US-10-791-619-12
                  prature:
    Namb/KEY: Artificial
    LOGATION: 1-114
    CTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-791-619-11
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Best Local Similarity 100.0%;
Matches 11; Conservative 0
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11, Conservative
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Sequence 2, Application US/10791619; Publication No. US20040259077A1; GENERAL INFORMATION:
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; Sequence 3, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
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                           26 GYSITSGYSWN 36
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US-10-791-619-2
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US-10-791-619-2
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 100.0%; Pred. No. 0.012;
tive 0; Mismatches 0; Indels
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; Publication No. US20030149244A1
GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Dardieu, Paula M.
APPLICANT: Jardieu, Paula M.
; APPLICANT: Jardieu, Paula M.
; TILE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT APPLICATION NUMBER: US 09/887,352
; PRIOR APPLICATION NUMBER: US 09/996,005
; PRIOR APPLICATION NUMBER: US 09/996,005
; PRIOR PILING DATE: 1999-04-21
; PRIOR FILING DATE: 1999-04-21
; PRIOR FILING DATE: 1999-04-21
; RUMBER OF SEQ ID NOS: 44
; SEQ ID NOS: 44
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 Best Local Similarity 100.
Matches 11, Conservative
                                                                      26 GYSITSGYSWN 36
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US-10-113-996-2
                                                                                                                                  RESULT 11
US-09-920-171-3
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US-10-113-996-2
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TITLE OF INVENTION: Leowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of Improving Polypeptides FILE REPERENCE: Pli2RI CURRENT PEPLICATION NUMBER: US/10/791,619
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/109,207
PRIOR PILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 2
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100.0%; Score 64; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: F(ab) sequence derived from MAE11
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Dresta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Improved Anti-IgE Antibodies
FILE REFERENCE: P12333US
CURRENT APPLICATION NUMBER: US/10/113,996
CURRENT FILING DATE: 2002-04-01
PRIOR PILING DATE: 1999-04-21
PRIOR PILING DATE: 1999-04-21
PRIOR PILING DATE: 1999-04-21
PRIOR PILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
SROID NOS: 44
SROID NOS: 44
LENGTH: 121
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US-10-791-619-3
; Sequence 3, Application US/10791619
; Publication No. US2004025907A1
; GRNERAL INFORMATION:
GRNERAL INFORMATION:
TILE REPRENENCE: Pl123R1
CURRENT PILLING DATE: 2004-03-02.07
; PRIOR PPLICATION NUBER: US/10/791,619
CURRENT PILLING DATE: 3096-05-30
; PRIOR PPLICATION NUBER: US/09/109,207
; PRIOR PILLING DATE: 1998-06-30
; PRIOR PILLING DATE: 1998-06-30
; PRIOR PILLING DATE: 1998-06-30
; PRIOR PILLING DATE: 1997-07-03
; PRIOR PILLING DATE: 199
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RESULT 2
US-11-136-250-10
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Sequence 10, Appli
Sequence 5, Appli
Sequence 50, Appl
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Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
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Sequence 19, Appl
Sequence 19, Appl
Sequence 21, Appl
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Sequence 22, Appl
Sequence 22, Appl
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                                                                                                                                 April 25, 2006, 07:01:21 ; Search time 7.0566 Seconds (without alignments) 68.593 Million cell updates/sec
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Sequence 34,
Sequence 71,
Sequence 49,
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1: /SIDS5/ptodata/1/pubpaa/US06_NEW_FUB.pep:*

2: /SIDS5/ptodata/1/pubpaa/US06_NEW_FUB.pep:*

3: /SIDS5/ptodata/1/pubpaa/US07_NEW_FUB.pep:*

4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_FUB.pep:*

5: /SIDS5/ptodata/1/pubpaa/US10_NEW_FUB.pep:*

7: /SIDS5/ptodata/1/pubpaa/US10_NEW_FUB.pep:*

7: /SIDS5/ptodata/1/pubpaa/US10_NEW_FUB.pep:*

8: /SIDS5/ptodata/1/pubpaa/US11_NEW_FUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-136-250-10

US-10-923-327-4

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US-11-208-422-50

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US-11-208-422-50

US-11-208-422-51

US-10-923-327-14

US-10-923-327-14

US-10-923-327-19

US-10-923-327-10

US-10-923-327-10

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US-11-208-33-79
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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26 54 84.4 121 6 US-10-946-836A-12 Sequence 12, Appl 27 48.4 121 6 US-10-988-207-12 Sequence 12, Appl 28 44.4 127 7 US-11-012-353-52 Sequence 52, Appl 30 54 84.4 135 7 US-11-012-353-77 Sequence 77, Appl 31 52 81.2 248 6 US-10-923-327-15 Sequence 81, Appl 32 52 81.2 248 6 US-10-923-327-15 Sequence 15, Appl 33 50 78.1 135 7 US-11-012-353-89 Sequence 16, Appl 34 50 78.1 135 7 US-11-012-353-89 Sequence 16, Appl 36 US-10-923-327-16 Sequence 16, Appl 36 US-10-923-327-16 Sequence 16, Appl 36 US-10-10-923-327-16 Sequence 16, Appl 36 To 135 7 US-11-012-353-89 Sequence 16, Appl 36 To 137 7 US-11-012-353-89 Sequence 16, Appl 37 48 75.0 98 7 US-11-012-353-74 Sequence 44, Appl 40 48 75.0 126 US-10-469-469-48 Sequence 36, Appl 41 48 75.0 126 US-10-469-469-36 Sequence 36, Appl 42 48 75.0 126 US-10-469-469-38 Sequence 36, Appl 44 48 75.0 126 US-10-469-469-38 Sequence 37, Appl 44 48 75.0 126 US-10-469-469-38 Sequence 38, Appl 44 48 75.0 126 US-10-469-469-38 Sequence 1548, Appl 44 48 75.0 126 US-10-469-48 Sequence 1548, Appl 44 48 75.0 126 US-10-469-469-48 Sequence
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# ALIGNMENTS

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US-11-084-554-10

Sequence 10, Application US/11084554

Publication No. US20050260679A1

Sequence 10, Application US/11084554

Publication No. US20050260679A1

Sequence 10, Application Sirid-A1

APPLICANT: Kellermann, Sirid-A1

APPLICANT: Kellermann, Sirid-A1

APPLICANT: Green, Wouter

TITLE OF INVERTION: ANTHEODIES THROUGH V GENE MANIPULATION

FILE RESERVE: ASSENTY.1004

CURRENT FILING DATE: 2005-03-17

FRIOR APPLICANTON NUMBER: 60/54,372

FRIOR APPLICANTON NUMBER: 60/54,372

FRIOR APPLICANTON NUMBER: 60/54,661

FRIOR APPLICANTON NUMBER: 60/54,661

FRIOR APPLICANTON NUMBER: 60/54,661

FRIOR APPLICANTON NUMBER: 60/54,661

FRIOR PILING DATE: 2004-03-19

FRIOR PILING DATE: 2004-03-19

FRIOR PILING DATE: 2004-05-34

FRIOR PILING DATE: 2004-05-34

FRIOR FILING DATE: 2004-05-34

GRESSIAL 1NFORMATION: SITIGA-A1

APPLICANT: GREEN, LAITY L.

FRESURT & CIVARYION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

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FILING OF INVERTION OF 100-05-23

CURRENT FILING DATE: 2006-05-23

CURRENT FILING DATE: 2006-05-23

FILING DATE: 2006-05-25-25

FILING DATE: 2006-05-25-25

FILING DATE: 2006-05-25-25

FILING DATE: 2006
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US-11-208-422-50
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LENGTH: 121
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| Sequence 4, Application US/10923327
| Sequence 4, Application Wo. US200562208A1
| GENERAL INFORMATION:
| APPLICANT: ROBINSON, CYNTHIA B. |
| APPLICANT: ROBINSON, CYNTHIA B. |
| TITLE OF INVENTION: DEHYDROEPIANDROSTERONB OR |
| TITLE OF INVENTION: DEHADOR FOR TREATHENT OF ASTHMA OR CHRONIC OBSTRUCTIVE |
| FILE REFERENCE: 30775-73.501 |
| CURRENT APPLICATION NUMBER: US/10/923,327 |
| CURRENT FILING DATE: 2004-09-20 |
| PRIOR FILING DATE: 2004-07-30 |
| PRIOR FILING DATE: 2003-07-31 |
| PRIOR FILING DATE: 2003-07-31 |
| NUMBER OF SEQ ID NOS: 19 |
| SEQ ID NO 4 |
| LEASTH: 114 |
| LEASTH: 114 |
| LEASTH: 114
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Sequence 5, Application US/10923327

Fublication No. US20050261208A1

GENERAL INFORMATION:

APPLICANT: ROBINSON, CYNTHIA B.

APPLICANT: BALL, HOWARD A.

TITLE OF INVENTION: COMBINATION OF DEHYDROEFIANDROSTERONE OR

TITLE OF INVENTION: DEHYDROEFIANDROSTERONE WITH AN ANTI-IGE

TITLE OF INVENTION: DEHYDROEFIANDROSTERONE-SULFATE WITH AN ANTI-IGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: construct
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                                                                                                                                                                                                                                                                                                                                                 Length 98;
                                                                                                                                                                                                                                                                                                                         Score 64; DB 7; Lengtn >v. Pred. No. 0.0012;
PRIOR FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: PCT/US2005/009306
PRIOR FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: 60/574,661
PRIOR APPLICATION NUMBER: 60/574,661
PRIOR PILING DATE: 2004-05-24
PRIOR PILING DATE: 2004-01-19
NUMBER OF SEQ ID NOS: 266
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 98
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Best Local Similarity 100.º
Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-11-136-250-10
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TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE TITLE OF INVENTION: PULMONARY DISEASE FILE REFERENCE: 30775-723.501
CURRENT APPLICATION NUMBER: US/10/923,327
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: PCT/US04/25054
PRIOR FILING DATE: 2004-07-30
PRIOR PLING DATE: 2003-10-29
PRIOR PLING DATE: 2003-10-29
PRIOR FILING DATE: 2003-07-31
NUMBER OF SQD 10 NOS: 19
SOFTWARE: PATENTIN Ver: 3.3
SEQ ID NO 5: 44
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APPLICANT: Adams, Camellia W.
APPLICANT: Lien, Samantha
APPLICANT: Lien, Samantha
APPLICANT: Lien, Samantha
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Marvin, Jonathan S.
APPLICANT: Meng, Yu-Ju G.
APPLICANT: LOWMER: US/11/208,422
CURRENT APPLICATION NUMBER: US/11/208,422
PRIOR APPLICATION NUMBER: US 60/603,057
PRIOR FILING DATE: 2004-08-19
NUMBER OF SEQ ID NOS: 54
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic;
; OTHER INFORMATION: construct
; OTHER INFORMATION: CONSTRUCT
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Best Local Similarity 100.0%; Score 64; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
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APPLICANT: AAGMS, Camellia W.
APPLICANT: Lien, Samantha APPLICANT: Lien, Samantha APPLICANT: Lowman, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-208-422-48
; Sequence 48, Application US/11208422
; Publication No. US20060067930A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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CURRENT FILING DATE: 2004-08-20
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US-10-923-327-18
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Sequence 13, Application US/10923327

Sequence 13, Application US/10923327

Sequence 13, Application US/10923327

Sequence 13, Application US/10923327

GENERAL INFORMATION:

APPLICANT: RALL, HOWARD A.

TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR

TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE

TITLE OF INVENTION: AUTHONARY DISEASE

TITLE OF INVENTION: AUTHONARY DISEASE

TITLE REFERENCE: 30775-723.501

CURRENT APPLICATION NUMBER: US/10/923,327
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; Sequence 52, Application No. US20060067930A1
; Publication No. US20060067930A1
; GENERAL INFORMATION:
    APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha S.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION FILE REFERENCE: P2158R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT PILING DATE: 2004-08-19
; RIOR PILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
APPLICANT: Marvin, Jonathan S.
APPLICANT: Meng, Yu-Ju G.
TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED BFFECTOR FUNCTION
FILE REPREBRIES: P2158H;
CURRENT APPLICATION NUMBER: US/11/208,422
CURRENT FILING DATE: 2005-08-19
PRIOR APPLICATION NUMBER: US 60/603,057
PRIOR APPLICATION NUMBER: US 60/603,057
PRIOR APPLICATION NUMBER: US 60/603,057
PRIOR PILING DATE: 2004-08-19
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 50
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100.0%; Score 64; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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; OTHER INFORMATION: sequence is synthesized
US-11-208-422-52
                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: sequence is synthesized US-11-208-422-50
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                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 11, Conservative
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LENGTH: 121
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Sequence 14, Application US/10923327

Sequence 14, Application US/20923327

Publication No. US20050261208A1

GENERAL INFORMATION:

APPLICANT: ROBINSON, CYNTHIA B.

APPLICANT: BALL, HOWARD A.

TITLE OF INVENTION: DEHYDROSPIANDROSTERONE OR

TITLE OF INVENTION: ANTIBODY FOR TREATHENT OF ASTHMA OR CHRONIC OBSTRUCTIVE

TITLE OF INVENTION: PULMONARY DISEASE

FILE REPRESENCE: 30775-723.501

CURRENT FILING DATE: 2004-08-20

PRIOR PILING DATE: 2004-07-30

PRIOR PPLICATION NUMBER: 10/698,073

PRIOR PILING DATE: 2003-07-31

NUMBER OF SEQ ID NOS: 19

SEQ ID NO 14

LENGTH: 229

LENGTH: 229

LENGTH: 229
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US-10-923-327-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 64; DB 6; Length 229; 100.0%; Pred. No. 0.0026; tive 0; Mismatches 0; Indels
PRIOR PELING DATE: 2004-07-30
PRIOR PELING DATE: 2004-07-30
PRIOR PELING DATE: 2004-07-30
PRIOR PELING DATE: 2003-10-29
PRIOR PELING DATE: 2003-10-29
PRIOR PELING DATE: 2003-07-31
PRIOR PILING DATE: 2003-07-31
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 13
LENGTH: 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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US-10-923-327-7
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WESULO 11

WESULO 11

Sequence 19, Application US/10923327

Sequence 19, Application US/10923327

PUBLICARIN NO. US2005261208A1

SEQUENCE INFORMATION:

APPLICANT: ROBINSON, CYNTHIA B.

APPLICANT: BALL, HOWAND A.

TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR

TITLE OF INVENTION: DEHYDROEPIANDROSTERONE OR

TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE

TITLE OF INVENTION: PULLOON FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE

TITLE OF INVENTION: PULLOON FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE

TITLE OF INVENTION: PULLOON FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE

FILE REFERENCE: 30775-723.501

CURRENT APPLICATION NUMBER: US/10/923,327

CURRENT FILING DATE: 2004-07-30

PRIOR PLLING DATE: 2004-07-30

PRIOR PLLING DATE: 2003-07-31

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PALEALIN VEY: 3.3

SEQ ID NO 19

LENGTH: 233

LENGTH: 233
           TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: ANTI-BODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
TITLE OF INVENTION: PULMONARY DISEASE
FILE REFERENCE: 30775-723.501
CURRENT PILING DATE: 2004-08-20
PRIOR PILING DATE: 2004-08-20
PRIOR PLING DATE: 2004-07-30
PRIOR PLING DATE: 2003-10-29
PRIOR PLING DATE: 2003-10-29
PRIOR PLING DATE: 2003-10-29
PRIOR PLING DATE: 2003-10-31
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VOT: 3.3
SEQ ID NO 18
LENGTH: 233
TYPE: PRI
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US-10-923-327-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: CONStruct US-10-923-327-18
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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BALL, HOWARD A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYSITSGYSWN 11
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APPLICANT: ROBINSON, CYNTHIA B.
APPLICANT: ROBINSON, CYNTHIA B.
APPLICANT: BALL, HOWARD A.
TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: DEHYDROBY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
FILE REFERENCE: 30775-723.501
CURRENT PILING DATE: 2004-08-20
CURRENT PILING DATE: 2004-07-30
PRIOR FILING DATE: 2004-07-30
PRIOR PLING DATE: 2003-07-31
PRIOR PILING DATE: 2003-07-31
PRIOR PILING DATE: 2003-07-31
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VEY: 3.3
SEQ ID NO 9
LENGTH: 451
                                                                                      APPLICANT: ROBINSON, CYNTHIA B.
APPLICANT: RALL, HOWARD A.
TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
TITLE OF INVENTION: DEHYDROSTERONE-SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE
TITLE OF INVENTION: PULL DEHYDROSTERONE OF ASTHWA OR CHRONIC OBSTRUCTIVE
TITLE OF INVENTION: PULLON FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE
TITLE OF INVENTION: DATE: 2004-08-20
CURRENT FILING DATE: 2004-08-20
CURRENT FILING DATE: 2004-07-30
PRIOR FILING DATE: 2004-07-30
PRIOR PLIING DATE: 2003-10-29
PRIOR FILING DATE: 2003-10-29
PRIOR PLIING DATE: 2003-10-29
PRIOR PLIING DATE: 2003-10-29
PRIOR PLIING DATE: 2003-07-31
SOPTWARE: PATENTION NUMBER: 60/492,231
NUMBER OF SEQ ID NOS: 19
SOPTWARE: PATENTION VET: 3.3
SSOPTWARE: PATENTIN VET: 3.3
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US-10-923-327-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: construct
US-10-923-327-7
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i. Sequence 9, Application US/10923327
i. Publication No. US20050261208A1
j. GENERAL INFORMATION:
Sequence 7, Application US/10923327
Publication No. US20050261208A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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Search completed: April 25, 2006, 07:10:00 Job time : 7.22327 secs
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                                                                                                                                                                                                                                                                                                                                                                               | Sequence 11. Application US/10923327 | Sequence 11. Application US/10923327 | Sequence 11. Application No. US2005026120841 | GENERAL INFORMATION: Publication No. US2005026120841 | GENERAL INFORMATION: PEDICANT: ROBINSON, CTNTHIA B. | APPLICANT: ROBINSON, CTNTHIA B. | APPLICANT: ROBINSON, CTNTHIA B. | TITLE OF INVENTION: DEHYDROBPLANDROSTERONE-SULFATE WITH AN ANTI-IGE | TITLE OF INVENTION: DHYDRORPLANDROSTERONE-SULFATE WITH AN ANTI-IGE | TITLE OF INVENTION: DHYDRORPLANDROSTERONE-SULFATE WITH AN ANTI-IGE | TITLE OF INVENTION: PULMONARY DISEASE | TITLE OF INVENTION: PULMONARY DISEASE | FILE REFERENCE: 30775-723.501 | CURRENT FILING DATE: 2004-08-20 | PRIOR APPLICATION NUMBER: PCT/US04/25054 | PRIOR APPLICATION NUMBER: 60/492,231 | PRIOR APPLICATION NUMBER: 60/492,231 | PRIOR PLING DATE: 2003-10-29 | PRIOR APPLICATION NUMBER: 60/492,231 | NUMBER OF SEQ ID NOS: 19 | SEQ ID NO 11 | LENGTH: 451 | TYPE: PRT | T
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US-11-208-422-20
is Sequence 20, Application US/11208422
is Publication No. US20060067930A1
is GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Lien, Samanthan S.
APPLICANT: Lien, Jonathan S.
APPLICANT: Maryin, Jonathan S.
APPLICANT: Maryin, Jonathan S.
APPLICANT: Maryin, Jonathan S.
APPLICANT: Maryin, Solathan S.
PILE REFERENCE: P2158R1
CURRENT FILING DATE: 2005-08-19
PRIOR PILING DATE: 2005-08-19
PRIOR PILING DATE: 2004-08-19
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 20
LENGTH: 451
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US-10-923-327-11
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Best Local Similarity 100.0%; Fred. No. 0.0047; Matches 11; Conservative 0; Mismatches 0; Indels
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COTHER INFORMATION: Sequence is synthesized US-11-208-422-20
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US-10-923-327-11
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Query Match
Best Local Similarity 100.0%; Score 64; DB 7; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 0; Indels
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26 GYSITSGYSWN 36

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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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sw model using - protein search, OM protein

Run on:

April 25, 2006, 06:05:16 ; Search time 53.3962 Seconds (without alignments) 82.286 Million cell updates/sec

US-10-764-428-14 58 score: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 GYTFTNYGIN 10 Scoring table: Seguence:

2443163 segs, 439378781 residues Searched: 2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003s:* geneseqp2004s:* A_Geneseq_21:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## OUTCOMPTO

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SUMMARIES		Ę		ADQ90710	AAW70684	AAW70680	AAB13383	ABP61249	ABP61253	ADO14132	ADQ90737	ADQ90732	ADQ90729	ADQ90731	ABR83196	ABR83194	ABR83198	ADU26544	ADU26540	ADU26548	AAW70611	AAG80311	ABP61180	ADR89785	AEA40554	AEA40550	ADH62639	
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ADH62638 ADH62637 ADX58481 ADX58482	ADX58483 AAW24529 AAU80997	AAU80980 AAB84740 AAB84739	AAE27830 AAE27839 AAE27837 AAE27825	AAE27826 AAE27828 AAE27832 AAE27834 ADG67541 ADG67537
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## ALIGNMENTS

ADQ90710 standard; peptide; 10 AA. RESULT 1 ADQ90710

ADQ90710;

(first entry) 21-OCT-2004 Anti-VEGF antibody heavy chain HVR1 peptide SEQ ID NO:14.

antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antiangiogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; andiogenic disorder; immunological disorder; anti-VEGF antibody; anti vascular endothelial cell growth factor antibody; heavy chain; HVR1. 

Homo sapiens Synthetic.

WO2004065417-A2.

05-AUG-2004.

23-JAN-2004; 2004WO-US001844.

23-JAN-2003; 2003US-0442484P.

(GETH ) GENENTECH INC.

Simmons L;

WPI; 2004-562149/54.

Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.

Claim 13, SEQ ID NO 14; 161pp; English

The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid

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with a corresponding HVR1 and/or HVR2 sequence of the variable domain.

The antibody or antigen binding fragment variable domain comprises the modified FR that has improved yield in cell culture compared to an unmodified antibody or antigen binding fragment. The antibody and antigen binding fragment. The antibody and antigen binding fragment The antibody herapy. The hinding fragment have cytostatic, antinflammatory, antianglogenic and immunomodulatory activities, and can be used in antibody therapy. The producing antibodies or antigen binding fragments in cell culture, in particular for improving the yield of recombinant antibodies or antigen binding fragment antibodies or antigen binding fragment antibodies or antigen bed to diagnose, treat, inhibit or prevent e.g. tumours and inflammatory, angiogenic and immunological disorders. The present caequence represents a heavy chain HVR1 peptide of an anti-VEGF (vascular endothelial cell growth factor) antibody, which is used in the exemplification of the present invention.
position with a different amino acid, where the different amino acid is the amino acid found at the corresponding FR position of a human subgroup variable domain consensus sequence that has a hypervariable region 1 (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
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Sequence 10 AA;

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    100.0%; Score 58; DB 8; Length 10; 100.0%; Pred. No. 0.013; ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.
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AAW70684 standard; peptide; 118 AA. (first entry) 27-JAN-1999 AAW70684; RESULT 2

Anti-VEGF humanised antibody variable heavy domain of variant Y0238-3. Heavy variable domain; murine; humanised antibody; anti-vascular endothelial growth factor antibody; anti-VEGF antibody; VEGF-induced angiogenesis; themour; retinal disorder: agg-related macular degeneration; diabetic retinopathy; rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

Synthetic. gb.

Homo sapiens

WO9845331-A2

15-0CT-1998.

97US-00833504. 37-APR-1997; 06-AUG-1997;

98WO-US006604.

03-APR-1998;

(GETH ) GENENTECH INC.

Chen YM Lowman HB, Presta LG, WPI; 1998-568337/48. Wells JA, Baca M,

New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.

Example 3; Fig 10B; 100pp; English

The present sequence represents a variable heavy domain of an affinity

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matured anti-vascular endothelial growth factor (anti-VEGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinopathy). They can also be used to treat other conditions that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-VEGF antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New humanised antibody with affinity for vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-VEGF humanised antibody variable heavy domain of variant Y0192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-vascular endothelial growth factor antibody; anti-VEGF antibo
VEGF-induced anglogenesis; tumour; retinal disorder;
age-related macular degeneration; diabetic retinopathy;
rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
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                                                                                                                                                                                                          100.0%; Score 58; DB 2; Length 118; 100.0%; Pred. No. 0.14; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy variable domain; murine; humanised antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAW70680 standard; peptide; 118 AA
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97US-00908469
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Matches 10; Conserv
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                                                                                                                                                                             Sequence 118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
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AAB13383;

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The present invention relates to humanised anti-VEGF (vascular endothelial growth factor) antibodies or a variant of a parent anti-VEGF antibodies are useful for inhibiting VEGF-induced angiogenesis in a mammal (particularly a human), particularly those having a tumour or a retinal disorder e.g. intraocular neovascular disorders. The present sequence is an exemplary heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized anti-VEGF (vascular endothelial growth factor) antibodies or their variants, useful for inhibiting VEGF-induced angiogenesis in a mammal, particularly for treating tumor or retinal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF; vascular endothelial growth factor; anglogeneals inhibitor; tumour; retinal disorder; intraocular neovascular disorder; Y0192; heavy chain; variable domain.
hybridoma cells and those with affinity for VEGF are identified by immunoprecipitation or by an in vitro binding assay
                                                                                               100.0%; Score 58; DB 3; Length 118; 100.0%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised anti-VEGP Y0192 antibody variable heavy domain.
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                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                   ABP61249 standard; protein; 118 AA.
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/label= CDR-H2
70. .79
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/label= CDR-H1
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/label= CDR-H3
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                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                             1 GYTFTNYGIN 10
                                                                                                                                                                                                                  GYTPTNYGIN 35
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PRESTA L G.
LOWMAN H B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002032315-A1.
                                                              Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                         ABP61249;
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(WELL/)
(PRES/)
(LOWM/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHEN/)
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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the heavy chain variable region of the affinity matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody Y0238-3. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may be used to treat conditions characterised by undesirable excessive necovascularisation. Such conditions include tumours (especially solid ones), rheumatoid arthritis, psoriasis, atheroscierosis, diabetes and cher retinopathies, retrolental fibroplasia, age-related macular degeneration, necvascular glaucoma, haemangiomas, thyroid hyperplasias and chronic inflammation. Oedemas associated with tumours, strokes and head trauma, and sacites associated with malignancies, meig's syndrome, humg inflammation, nephrotic syndrome, pericardial effusion and pleural effusion, may also be treated. Monoclonal antibodies are generated in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and chronic inflammation in a mammal, comprises administering a human vascular endothelial cell growth factor antagonist.
                                                                                                                                                                                                                                                                                                                                                                        YO243-1; vascular endothelial cell growth factor; VEGF; antibody; antinflammatory; cerebroprotective; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic; antichyroid; excessive neovascularisation; tumour; rheumatoid arthritis; psoriasis, atherosclerosis, diabetes; retrolental fibroplasia; neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease; tissue transplantation; inflammation; oedema; trauma;
                                                Gaps
                                                ö
        100.0%; Score 58; DB 2; Length 118; 100.0%; Pred. No. 0.14; ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                             Anti-VEGF antibody YO238-3 heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 14B; 60pp; English
                                                                                                                                                                                                                            AAB13383 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50. .66
/label= CDR-H2
70. .79
/label= CDR-7
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/label= CDR-H1
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/label= CDR-H3
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                                                                                                                                                                                                                                                                                                       21-NOV-2000 (first entry)
          Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                         GYTFTNYGIN 10
                                                                                                                         GYTPTNYGIN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
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29-JUN-2000

Region Region Region Region Chen YM;

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Gaps

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Length 118; 0; Indels

Score 58; DB 5; Pred. No. 0.14; 0; Mismatches

100.0%;

Conservative

(first entry)

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Plasmid pxVG11VNERK expression cassette heavy chain protein SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; variant heavy chain hinge region; immunoconjugate; cytostatic; immunosuppressive; immunotherapy; tumour; cancer; immune disorder; expression cassette; plasmid pxVG11VNERK; anti-VEGF heavy chain.
                                                                                                                                                                                                                                                                             ADO14132 standard; protein; 479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-OCT-2003; 2003WO-US034610.
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                                                                                                                                     1 GYTFTNYGIN 10
                                                                                                                                                          GYTFTNYGIN 35
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                                  Query Match
Best Local Similarity
                  Sequence 118 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic, ophthalmological; humanised; antibody; anti-VEGF; VEGF; vascular endothelial growth factor; angiogenesis inhibitor; tumour; retinal disorder; intraocular neovascular disorder; Y0238-3; heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New humanized anti-VEGF (vascular endothelial growth factor) antibodies or their variants, useful for inhibiting VEGF-induced angiogenesis in a mammal, particularly for treating tumor or retinal disorders.
                                                                                                                   Gaps
variable domain of the humanised anti-VEGF antibody of the invention
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                                                                          Length 118;
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                                                                        100.0%; Score 58; DB 5;
100.0%; Pred. No. 0.14;
ive 0; Mismatches
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/label= CDR-H1
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/label= CDR-H2
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/label= CDR-H3
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/label= CDR-7
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                   Conservative
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WELLS J A.
PRESTA L G.
LOWMAN H B.
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                                                                   Query Match
Best Local Similarity
Matches 10; Conserv
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                                     Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variable domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
Synthetic.
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(WELL/) V
(PRES/) I
(LOWM/) I
(CHEN/) C
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                                                                                                                                                                                                                                                             RESULT 6
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ABP AC ABP 6125;

ABP AC ABP 6125;

ABP AC ABP AC ABP 6125;

ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC ABP AC 
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The present invention describes an antibody comprising a variant heavy chain hinge region incapable of inter-heavy chain disulfide linkage. Also described: (1) an antibody lacking inter-heavy chain disulfide linkage. Also (2) an immunoconjugate comprising the antibody conjugated with a cherologous moiety; (3) a composition comprising the antibody or immunoconjugate, and carrier; (4) an article of manufacture comprising the composition in a container; (5) a polymucleotide encoding the antibody or immunoconjugate, or a variant immunoglobulin heavy chain cantibody or immunoconjugate; (6) a polymucleotide encoding the comprising the recombinant vector; (8) expressing in a host cell comprising the recombinant at least one inter-heavy chain disulfide linkage; (6) a recombinant comprising the recombinant at least one inter-heavy chain disulfide linkage; (6) an approsylated antibody produced by the method; and (10) treating, clinkage is eliminated, and recovering the antibody from the host cell; (7) an aglycosylated antibody produced by the method; and (10) treating, preventing, diagnosing, delaying or preventing, diagnosing, delaying or preventing a disease in a subject. The antibody preventing, diagnosing, diagnosing, delaying or preventing a disease, e.g. tumour, cancer or immune disorder. The present sequence represents the anti-VEGF heavy chain from the expression cassette of the present function of the present function of the present function of the present function of the capacity or preventing the anti-VEGF heavy chain from the expression cassette of the present function of the capacity or preventing the function of the present function of the capacity or preventing the function of the expression cassette.
                                                                                                                                                                                  New antibody comprising a variant heavy chain hinge region incapable of inter-heavy chain disulfide linkage, useful for treating, preventing, diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 12; 124pp; English.
WPI; 2004-390607/36.
                                                                       N-PSDB; ADO14130.
                                                                                                                                                                                                                                                                                                                                                                                                                      immune disorder.
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The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid to position with a different amino acid, where the different amino acid is constituted found at the corresponding FR position of a human subgroup variable domain consensus sequence that has a hypervariable region 1 (HVR1) and/or HVR2 amino acid sequence with the most sequence identity variable domain comprises the modified FR that has improved Yield in cell culture compared to an modified antibody or antigen-binding fragment. The antibody and antigen binding fragment. The antibody and antigen commodified antibodies or antigen-binding fragment. The antibody and antigen methods and compositions of the present invention are useful for particular for improving the Yield of recombinant antibodies or antigen binding fragments in cell culture, in particular for improving the Yield of recombinant antibodies or antigen binding fragments of the invention can be ö Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell. antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antiinflammatory; antiangiogenic; immunomdulatory; antibody therapy; tumour; inflammatory disorder; anglogenic disorder; immunological disorder; anti-VEGF antibody; anti-vascular endothelial cell growth factor antibody; heavy chain. Gaps ö 100.0%; Score 58; DB 8; Length 479; 100.0%; Pred. No. 0.56; cive 0; Mismatches 0; Indels Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:21. Example 7; SEQ ID NO 27; 161pp; English. ADQ90737 standard; protein; 479 AA. 23-JAN-2004; 2004WO-US001844. 23-JAN-2003; 2003US-0442484P (first entry) Local Similarity 100 1es 10; Conservative 1 GYTFTNYGIN 10 58 (GETH ) GENENTECH INC WPI; 2004-562149/54. 49 GYTFTNYGIN N-PSDB; ADQ90722 Sequence 479 AA; WO2004065417-A2. Homo sapiens 21-OCT-2004 05-AUG-2004 Simmons L; Synthetic ADQ90737; Query Match Matches RESULT 8 ADQ90737 g ਨੇ 셤

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The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antigen binding fragment comprises expressing a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the antibody or antigen binding fragment variable domain comprising the author described above has a substitution of at least one amino acid to position with a different amino acid, where the different amino acid is position with a different amino acid, where the different amino acid is constituted found at the corresponding FR position of a human subgroup variable domain consensus sequence that has a hypervariable region 1 (HYR1) and/or HYR2 amino acid sequence with the most sequence identity ith a corresponding HYR1 and/or HYR2 sequence of the variable domain.

The antibody or antigen binding fragment variable domain comprises the modified FR that has improved yield in cell culture compared to an entigen antibody or antigen-binding fragment. The antibody and antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.
used to diagnose, treat, inhibit or prevent e.g. tumours and inflammatory, anglogenic and immunological disorders. The present sequence represents the heavy chain of an anti-VEGF (vascular endothelial cell growth factor) antibody, which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified framework region; hypervariable region; cytostetic; antiinflammatory; antianglogenic; immunomodulatory; antibody therapy; tumour; inflammatory; disorder; angiogenic disorder; immunological disorder; anti-VEGF antibody; antibody; anti-vascular endothelial cell growth factor antibody; heavy chain.
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen binding fragment; cell culture; variable domain;
                                                                                                                                                                                                      ö
                                                                                                                                                                 8; Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:11.
                                                                                                                                                                                                      0; Indels
                                                                                                                                                                 100.0%; Score 58; DB 8; 100.0%; Pred. No. 0.56;
                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          ADQ90732 standard; protein; 479 AA.
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                                                                                                                                                                                                                                                                      GYTFTNYGIN 58
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N-PSDB; ADQ90706.
                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                        present invention
                                                                                                                           Sequence 479 AA;
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Synthetic.
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variable domain consensus sequence that has a hypervariable region 1

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binding fragment have cytostatic, antiinflammatory, antiangiogenic and immunomodulatory activities, and can be used in antibody therapy. The methods and compositions of the present invention are useful for producing antibodise or antigen binding fragments in cell culture, in particular for improving the yield of recombinant antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and inflammatory, angiogenic and immunological disorders. The present sequence represents the heavy chain of an anti-VEGF (vascular endothelial cell growth factor) antibody, which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid position with a different amino acid, where the different amino acid is the amino acid is the amino acid the amino acid is the amino acid found at the corresponding FR position of a human subgroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified framework region; hypervariable region; cytostatic; antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy; tumour; inflammatory; disorder; angiogenic disorder; immunological disorder; anti-VEF antibody; anti vascular endothelial cell growth factor antibody; heavy chain.
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody; antigen binding fragment; cell culture; variable domain;
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                                                                                                                                                                                                                                                                                 8; Length 479;
                                                                                                                                                                                                                                                    100.0%; Score 58; DB 8; Lenguarion 0%; Pred. No. 0.56; or Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 5; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ90729 standard; protein; 479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-2004; 2004WO-US001844.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                     58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region in a host cell.
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                                                                                                                                                                                                                                                                                                                                                                                                   GYTFINYGIN
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                                                                                                                                                                                                       present invention
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                                                                                                                                                                                                                                            Sequence 479 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADQ90729;
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(HYR1) and/or HYR2 amino acid sequence with the most sequence identity with a corresponding HYR1 and/or HYR2 sequence of the variable domain.

With a corresponding HYR1 and/or HYR2 sequence of the variable domain.

The antibody or antigen binding fragment variable domain comprises the modified FR that has improved yield in cell culture compared to an unmodified antibody or antigen-binding fragment. The antibody and antigen binding fragment have eytostatic, antiinflammatory, antianglogenic and immunomodulatory activities, and can be used in antibody therapy. The methods and compositions of the present invention are useful for producing antibodies or antigen binding fragments in cell culture, in particular for improving the yield of recombinant antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and can be inflammatory, angiogenic and immunological disporders. The present sequence represents the heavy chain of an anti-VEGF (vascular endothalial sequence represents) antibody, which is used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified framework region; hypervariable region; cytostatic; antiinflammatory; antiangiogenic; immunomodilatory; antibody therapy; tumour; inflammatory; disorder; angiogenic disorder; immunological disorder; anti-vese anti-ves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 58; DB 8; Length 479; 100.0%; Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity luv.
Labes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYTFTNYGIN 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 479 AA;
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recovering the antibody or antigen binding fragment variable domain comprising the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid position with a different amino acid, where the different amino acid is the amino acid found at the corresponding FR position of a human subgroup the amino acid found at the corresponding FR position of a human subgroup or variable domain consensus sequence that has a hypervariable region. It (HVR1) and/or HVR2 samino acid sequence with the most sequence identity with a corresponding HVR1 and/or HVR2 sequence of the variable domain. Complied FR that has improved yield in cell culture compared to an unaddified antibody or antigen-binding fragment. The antibody and antigen binding fragment. The antibody and antigen binding fragment and compositions of the present invention are useful for methods and compositions of the present invention are useful for producing antibodies or antigen binding fragments in cell culture, in particular for improving the yield of recombinant antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and cinflammatory, anglogenic and immunological disorders. The present sequence represents the heavy chain of an anti-VBGF (vascular endothelial sequence represents the heavy chain of an anti-VBGF (vascular endothelial
comprising a modified framework region (FR) in a host
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Sequence 479 AA;
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100.0%; Score 58; DB 8; Length 479; 100.0%; Pred. No. 0.56;
                     0; Indels
                      Mismatches
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0
         Local Similarity 100
   Query Match
                       Matches
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RESULT 12

ABR83196 standard; protein; 120 AA. ABR83196; **ABR**83196 

(first entry) 15-JAN-2004 Chimeric LL1 antibody heavy chain variable region (cLL1VH)

LL1; anti-CD74 antibody; CD-74; cytostatic; immunosuppressive; immunosuppressive; immunomodulator; cLL1; chimeric.

Chimeric - Mus sp.

WO2003074567-A2.

12-SEP-2003.

03-MAR-2003; 2003WO-GB000890

01-MAR-2002; 2002US-0360259P.

(IMMU-) IMMUNOMEDICS INC. (MCCA/) MCCALL J D.

Goldenberg DM; , g Hansen H, Leung S,

WPI; 2003-767381/72. N-PSDB; ACF57896

New humanized, human or chimeric anti-CD74 antibody or fragment, useful for diagnosing or treating a CD74 expressing malignancy, an immune dysregulation disease, an autoimmune disease or graft versus host

Claim 13; Fig 2A; 91pp; English

disease.

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The invention relates to a humanized, human or chimeric anti-CD74
antibody or its fragment. The naked anti-CD74 antibody or a naked
antibody fusion protein or fragment, or a therapeutic or diagnostic
conjugate comprising an anti-CD74 antibody is useful for diagnosting
conjugate comprising an anti-CD74 antibody is useful for diagnosting or
treating a disorder or a disease that is a CD74 expressing malignancy
c (solid tumour, non-Hodgkin's lymphoma, Hodgkin's lymphoma, multiple
myeloma, another B-cell malignancy and a T-cell malignancy), an immune
c graft versus host disease. The solid tumour is melanoma, carcinoma and
sarcoma. The arcinoma is a renal carcinoma, lung carcinoma and
c arcinoma, stomach carcinoma and melanoma. The B-cell malignancy is of
non-Hodgkin's lymphoma, Hodgkin's lymphomas, indolent forms of B-cell
lymphomas, aggressive forms of B-cell lymphomas, chronic lymphatic
leukemiss, acute lymphatic leukemias, and multiple myeloma. The present
sequence represents a chimeric anti-CD74 antibody LL1 (cLL1) heavy chain
variable region
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                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LL1; anti-CD74 antibody; CD-74; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                        DB 7; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Pred. No. 0.21;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                           Similarity 90.0
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunomodulator; mLL1
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                                                                                                                                                                                                                                                                                                                         Sequence 120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
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Best Local
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ID ABRE
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dysregulation disease, an autoimmune disease, organ graft rejection, and graft versus host disease. The solid tumour is melanoma, carcinoma and sarcoma. The carcinoma is a renal carcinoma, lung carcinoma, intestinal carcinoma, stomach carcinoma and melanoma. The B-cell malignancy is of non-Hodgkin's lymphoma, Hodgkin's lymphoma, indolent forms of B-cell lymphomas, aggressive forms of B-cell lymphomas, chronic lymphatic leukemias, acute lymphatic leukemias, and multiple myeloma. The present sequence represents a murine anti-CD74 antibody LL1 heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a humanised, human or chimeric anti-CD74 antibody or its fragment. The naked anti-CD74 antibody or a naked antibody or its fragment. The naked antibody or a naked antibody is useful for diagnostic conjugate comprising an anti-CD74 antibody is useful for diagnostic freating a disorder or a disease that is a CD74 expressing malignancy (solid tumour, non-Hodgkin's lymphoma, Hodgkin's lymphoma, multiple myeloma, another B-cell malignancy and a T-cell malignancy), an immune disease, an autoimmune disease, organ graft rejection, and graft versus host disease. The solid tumour is melanoma, carcinoma and sarcoma. The carcinoma is a renal carcinoma. The B-cell malignancy is of non-Hodgkin's lymphoma, Hodgkin's lymphoma, Hodgkin's lymphoma, Hodgkin's lymphoma, independent is a renal lymphomas, chronic lymphatic leukemias, and multiple myeloma. The present leukemias, acute lymphatic leukemias, and multiple myeloma. The present
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                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LL1; anti-CD74 antibody; CD-74; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised LL1 antibody heavy chain variable region (hLL1VH)
                                                                                                                                                                                                                           Score 57; DB 7; Length 120;
Pred. No. 0.21;
                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR83198 standard; protein; 120 AA.
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                                                                                                                                                                                                                         98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 90.v.
9, Conservative
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                                                                                                                                                                                                                                                                                                       1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                          26 GYTFTNYGVN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunomodulator; hLL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-767381/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MCCA/) MCCALL J D.
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                                                                                                                                                                                          Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003074567-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hansen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR83198;
                                                                                                                                                         region
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sequence represents a humanised anti-CD74 antibody LL1 (hLL1) heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressive; cytostatic; immunomodulatory; immunotoxin; radioimmunotherapeutic; immunoconjugate; anti-CD744 antibody; CD74-expressing malignancy; immune dysregulation disease; autoimmune disease; organ-graft rejection; graft-versus-host disease; solid tumor; non-Hodgkin's lymphoma; Hodgkin's lymphoma; multiple myeloma; B-cell malignancy; T-cell malignancy; melanoma; carcinoma; sarcoma; glioma; mouse; LL1; heavy chain variable region;
                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Complementarity determining region 2"
                                                                                                                                      Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric LL1 antibody heavy chain variable region segid 6.
                                                                                                                                                                                               Indels
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                                                                                                                                      Score 57; DB 7;
Pred. No. 0.21;
                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADU26544 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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2003US-00350096.
2003US-00377122.
2003US-0478830P.
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2001US-00965796.
2002US-0360259P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50. .66
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-2003; 2003US-00706852
                                                                                                                                         98.3%;
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/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99. .109
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-2005 (first entry)
                                                                                                                                                                                                 9; Conservative
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                                                                                                                                                                                                                                                    1 GYTFTNYGIN 10
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N-PSDB; ADU26543.
                                                                                                                                      Query Match
Best Local Similarity
                                                                                       Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2004219203-A1
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03-MAR-2003;
17-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-DEC-2002
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Region
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polymeric carriers, and effectors.

Disclosure; SEQ ID NO 6; 44pp; English.

The invention describes a composition (I) comprising an immunoconjugate which has one or more anti-CD74 binding molecules conjugated to one or more lapids, polymeric carriers, micelles, nanoparticles or their conbinations, and one or more effectors. Also described are: preparing combinations, and one or more effectors. Also described are: preparing combinations, and one or more effectors. Also described are: preparing combinations, and one or more effectors with an anti-CD744 antibody; and a kit comprising (I). (I) is useful for treating and/or antibody; and a carrier, and contacting the carrier with an anti-CD744 carrier of a graft-versus-host disease. The CD74-expressing malignancy, immune dysregulation disease. The CD74-expressing malignancy is of CD74-expressing malignancy is a Solid tumor. Which is chosen from and graft-versus-host disease. The CD74-expressing malignancy is a solid tumor, which is chosen from melanoma, carcinoma, proceed is CD74-expressing malignancy is a solid tumor, which is chosen from melanoma, prostate cancer, ovarian cancer, and melanoma. The CD74-expressing malignancy is a solid tumor, which is chosen from melanoma, prostate cancer, ovarian cancer, and melanoma. The CD74-expressing malignancy is a solid tumor, which is chosen from comparises LIJ or its fragment. The composition further comprises one or composition further comprises one or more additional antibodies or their fragments chosen from anti-CD19, anti-CD2, anti-CD3, anti-CD3, anti-CD3, anti-CD3, anti-CD2, anti-CD2, anti-CD2, anti-CD3, anti-CD 

Sequence 120 AA;

0; Gaps 98.3%; Score 57; DB 9; Length 120; 90.0%; Pred. No. 0.21; ive 1; Mismatches 0; Indels Query Match Best Local Similarity 90.0 Matches 9; Conservative

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1 GYTFTNYGIN 10

Search completed: April 25, 2006, 06:15:04 Job time : 55.3962 secs

26 GYTPTNYGVN 35 ઠે 셤

